OM protein - protein search, using sw model

Run on: August 28, 2003, 18:02:01 ; Search time 18 Seconds
(without alignments)
669.922 Million cell updates/sec

Title: US-09-507-968D-2
Perfect score: 1451
Sequence: 1 MDDSTEREQSRLTSCLKKRE.....ENAQISLDGDVTFFGALKLL 285

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1451	100.0	285	3	US-09-286-529-1	Sequence 1, Appli
2	1451	100.0	285	4	US-09-589-287B-2	Sequence 2, Appli
3	1451	100.0	285	4	US-09-496-118B-1	Sequence 1, Appli
4	1451	100.0	285	4	US-09-565-423-2	Sequence 2, Appli
5	1451	100.0	285	4	US-09-879-919-23	Sequence 23, Appl
6	1451	100.0	285	4	US-09-588-947A-2	Sequence 2, Appli
7	1335.5	92.0	266	4	US-09-589-287B-19	Sequence 19, Appl
8	1335.5	92.0	266	4	US-09-879-919-24	Sequence 24, Appl
9	1335.5	92.0	266	4	US-09-588-947A-19	Sequence 19, Appl
10	1080	74.4	219	4	US-09-589-287B-28	Sequence 28, Appl
11	1080	74.4	219	4	US-09-588-947A-28	Sequence 28, Appl
12	1074	74.0	219	4	US-09-589-287B-30	Sequence 30, Appl
13	1074	74.0	219	4	US-09-588-947A-30	Sequence 30, Appl
14	901	62.1	174	4	US-09-496-118B-5	Sequence 5, Appli
15	793	54.7	289	4	US-09-589-287B-38	Sequence 38, Appl
16	793	54.7	289	4	US-09-588-947A-38	Sequence 38, Appl
17	749	51.6	145	3	US-09-286-529-21	Sequence 21, Appl
18	579	39.9	155	4	US-09-589-287B-23	Sequence 23, Appl
19	579	39.9	155	4	US-09-588-947A-23	Sequence 23, Appl
20	244.5	16.9	250	3	US-08-883-086-2	Sequence 2, Appli
21	244.5	16.9	250	4	US-09-565-423-3	Sequence 3, Appli
22	243.5	16.8	233	4	US-10-082-260-2	Sequence 2, Appli
23	243.5	16.8	233	4	US-08-815-783-2	Sequence 2, Appli
24	243.5	16.8	233	4	US-09-879-919-2	Sequence 2, Appli
25	243.5	16.8	250	3	US-09-153-927-4	Sequence 4, Appli
26	243.5	16.8	250	4	US-09-879-919-11	Sequence 11, Appl
27	236.5	16.3	234	4	US-09-157-864-2	Sequence 2, Appli
28	236.5	16.3	247	4	US-09-157-864-4	Sequence 4, Appli
29	235.5	16.2	234	4	US-09-879-919-13	Sequence 13, Appl
30	231	15.9	46	4	US-09-496-118B-2	Sequence 2, Appli
31	229.5	15.8	205	3	US-09-286-529-5	Sequence 5, Appli
32	221.5	15.3	168	4	US-10-082-260-4	Sequence 4, Appli
33	221.5	15.3	168	4	US-08-815-783-4	Sequence 4, Appli
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35	213.5	14.7	147	3	US-08-883-086-3	Sequence 3, Appli
36	210	14.5	136	4	US-09-589-287B-20	Sequence 20, Appl
37	210	14.5	136	4	US-09-588-947A-20	Sequence 20, Appl
38	172	11.9	34	4	US-09-496-118B-4	Sequence 4, Appli
39	147	10.1	31	4	US-09-496-118B-3	Sequence 3, Appli
40	109.5	7.5	235	3	US-08-883-086-7	Sequence 7, Appli
41	104.5	7.2	163	1	US-07-994-469A-64	Sequence 64, Appl
42	102.5	7.1	391	4	US-09-342-681C-2	Sequence 2, Appli
43	102	7.0	204	4	US-08-815-783-6	Sequence 6, Appli
44	101.5	7.0	155	1	US-07-994-469A-67	Sequence 67, Appl
45	101.5	7.0	155	1	US-07-994-469A-68	Sequence 68, Appl

ALIGNMENTS

RESULT 1
US-09-286-529-1
; Sequence 1, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286,529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 285
; TYPE: PRT
; ORGANISM: human
US-09-286-529-1

Query Match 100.0%; Score 1451; DB 3; Length 285;
Best Local Similarity 100.0%; Pred. No. 7e-160;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-09-589-287B-2
; Sequence 2, Application US/09589287B
; Patent No. 6403770
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Antibodies to Neutrokine-alpha

```
;  FILE REFERENCE: PF343P3C1
;  CURRENT APPLICATION NUMBER: US/09/589,287B
;  CURRENT FILING DATE:  2000-06-08
;  Prior application data removed - check PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 285
;   TYPE: PRT
;   ORGANISM: human
US-09-589-287B-2

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RESULT 3
US-09-496-118B-1
; Sequence 1, Application US/09496118B
; Patent No. 6475986
; GENERAL INFORMATION:
;  APPLICANT:  Aggarwal, Bharat B.
;  TITLE OF INVENTION:  Uses of THANK, a TNF homologue that Activates
;  TITLE OF INVENTION:  Apoptosis
;  FILE REFERENCE:  D6206
;  CURRENT APPLICATION NUMBER: US/09/496,118B
;  CURRENT FILING DATE:  2000-02-01
;  PRIOR APPLICATION NUMBER:  US 60/118,531
;  PRIOR FILING DATE:  1999-02-02
;  NUMBER OF SEQ ID NOS:  13
; SEQ ID NO 1
;   LENGTH: 285
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: amino acid sequence of THANK protein
US-09-496-118B-1

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Qy        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
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Qy        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240
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RESULT 4
US-09-565-423-2
; Sequence 2, Application US/09565423
; Patent No. 6475987
; GENERAL INFORMATION:
;  APPLICANT:  Shu, Hong-Bing
;  TITLE OF INVENTION:  TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE:  2879-72
;  CURRENT APPLICATION NUMBER: US/09/565,423
;  CURRENT FILING DATE:  2000-05-05
;  PRIOR APPLICATION NUMBER:  UNKNOWN
;  PRIOR FILING DATE:  2000-05-01
;  PRIOR APPLICATION NUMBER:  60/132,892
;  PRIOR FILING DATE:  1999-05-06
;  NUMBER OF SEQ ID NOS:  17
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 285
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:primer
US-09-565-423-2

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Db          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60

Qy         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120
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Db         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120

Qy        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
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RESULT 5
US-09-879-919-23
; Sequence 23, Application US/09879919
; Patent No. 6541224
; GENERAL INFORMATION:
;  APPLICANT: Yu, Guo-Liang, et al.
;  TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
;  FILE REFERENCE: PF253P1
;  CURRENT APPLICATION NUMBER: US/09/879,919
;  CURRENT FILING DATE:  2001-06-14
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
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;  PRIOR APPLICATION NUMBER: 60/277,978
;  PRIOR FILING DATE: 2001-03-23
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/254,875
;  PRIOR FILING DATE: 2000-12-13
;  PRIOR APPLICATION NUMBER: 60/241,952
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/211,537
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 08/815,783
;  PRIOR FILING DATE: 1997-03-12
;  PRIOR APPLICATION NUMBER: 60/016,812
;  PRIOR FILING DATE: 1996-03-14
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
;   LENGTH: 285
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-879-919-23

  Query Match             100.0%;  Score 1451;  DB 4;  Length 285;
  Best Local Similarity   100.0%;  Pred. No. 7e-160;
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Qy        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
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Qy        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240
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Db        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285


RESULT 6
US-09-588-947A-2
; Sequence 2, Application US/09588947A
; Patent No. 6562579
; GENERAL INFORMATION:
;  APPLICANT: Yu et al.
;  TITLE OF INVENTION: Diagnostic Methods Using Antibodies to Neutrokine-alpha
;  FILE REFERENCE: PF343P3C2
;  CURRENT APPLICATION NUMBER: US/09/588,947A
;  CURRENT FILING DATE:  2000-06-08
;  PRIOR APPLICATION NUMBER: 09/588,947
;  PRIOR FILING DATE: 2000-06-08
;  PRIOR APPLICATION NUMBER: 09/507,968
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: 60/122,388
;  PRIOR FILING DATE: 1999-03-02
;  PRIOR APPLICATION NUMBER: 60/124,097
;  PRIOR FILING DATE: 1999-03-12
;  PRIOR APPLICATION NUMBER: 60/126,599
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: 60/127,598
;  PRIOR FILING DATE: 1999-04-02
;  PRIOR APPLICATION NUMBER: 60/130,412
;  PRIOR FILING DATE: 1999-04-16
;  PRIOR APPLICATION NUMBER: 60/130,696
;  PRIOR FILING DATE: 1999-04-23
;  PRIOR APPLICATION NUMBER: 60/131,278
;  PRIOR FILING DATE: 1999-04-27
;  PRIOR APPLICATION NUMBER: 60/131,673
;  PRIOR FILING DATE: 1999-04-29
;  PRIOR APPLICATION NUMBER: 60/136,784
;  PRIOR FILING DATE: 1999-05-28
;  PRIOR APPLICATION NUMBER: 60/142,659
;  PRIOR FILING DATE: 1999-07-06
;  PRIOR APPLICATION NUMBER: 60/145,824
;  PRIOR FILING DATE: 1999-07-27
;  PRIOR APPLICATION NUMBER: 60/167,239
;  PRIOR FILING DATE: 1999-11-24
;  PRIOR APPLICATION NUMBER: 60/168,624
;  PRIOR FILING DATE: 1999-12-03
;  PRIOR APPLICATION NUMBER: 60/171,108
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: 60/171,626
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: 60/176,015
;  PRIOR FILING DATE: 2000-01-14
;  PRIOR APPLICATION NUMBER: 09/255,794
;  PRIOR FILING DATE: 1999-02-23
;  PRIOR APPLICATION NUMBER: 09/005,874
;  PRIOR FILING DATE: 1998-01-12
;  PRIOR APPLICATION NUMBER: 60/036,100
;  PRIOR FILING DATE: 1997-01-14
;  PRIOR APPLICATION NUMBER: PCT/US96/17957
;  PRIOR FILING DATE: 1996-10-25
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 285
;   TYPE: PRT
;   ORGANISM: human
US-09-588-947A-2

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Db        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285


RESULT 7
US-09-589-287B-19
; Sequence 19, Application US/09589287B
; Patent No. 6403770
; GENERAL INFORMATION:
;  APPLICANT: Yu et al.
;  TITLE OF INVENTION: Antibodies to Neutrokine-alpha
;  FILE REFERENCE: PF343P3C1
;  CURRENT APPLICATION NUMBER: US/09/589,287B
;  CURRENT FILING DATE:  2000-06-08
;  Prior application data removed - check PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 42
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;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
;   LENGTH: 266
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-589-287B-19

  Query Match             92.0%;  Score 1335.5;  DB 4;  Length 266;
  Best Local Similarity   93.3%;  Pred. No. 1.6e-146;
  Matches  266;  Conservative    0;  Mismatches    0;  Indels   19;  Gaps    1;

Qy          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60

Qy         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120

Qy        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
              ||||||||||||||||||||                  ||||||||||||||||||||
Db        121 GEGNSSQNSRNKRAVQGPEET------------------GSYTFVPWLLSFKRGSALEE 161

Qy        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 221

Qy        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
              |||||||||||||||||||||||||||||||||||||||||||||
Db        222 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 266


RESULT 8
US-09-879-919-24
; Sequence 24, Application US/09879919
; Patent No. 6541224
; GENERAL INFORMATION:
;  APPLICANT: Yu, Guo-Liang, et al.
;  TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
;  FILE REFERENCE: PF253P1
;  CURRENT APPLICATION NUMBER: US/09/879,919
;  CURRENT FILING DATE:  2001-06-14
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,978
;  PRIOR FILING DATE: 2001-03-23
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/254,875
;  PRIOR FILING DATE: 2000-12-13
;  PRIOR APPLICATION NUMBER: 60/241,952
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/211,537
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 08/815,783
;  PRIOR FILING DATE: 1997-03-12
;  PRIOR APPLICATION NUMBER: 60/016,812
;  PRIOR FILING DATE: 1996-03-14
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
;   LENGTH: 266
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-879-919-24

  Query Match             92.0%;  Score 1335.5;  DB 4;  Length 266;
  Best Local Similarity   93.3%;  Pred. No. 1.6e-146;
  Matches  266;  Conservative    0;  Mismatches    0;  Indels   19;  Gaps    1;

Qy          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60

Qy         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120

Qy        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
              ||||||||||||||||||||                  ||||||||||||||||||||
Db        121 GEGNSSQNSRNKRAVQGPEET------------------GSYTFVPWLLSFKRGSALEE 161

Qy        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 221

Qy        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
              |||||||||||||||||||||||||||||||||||||||||||||
Db        222 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 266


RESULT 9
US-09-588-947A-19
; Sequence 19, Application US/09588947A
; Patent No. 6562579
; GENERAL INFORMATION:
;  APPLICANT: Yu et al.
;  TITLE OF INVENTION: Diagnostic Methods Using Antibodies to Neutrokine-alpha
;  FILE REFERENCE: PF343P3C2
;  CURRENT APPLICATION NUMBER: US/09/588,947A
;  CURRENT FILING DATE:  2000-06-08
;  PRIOR APPLICATION NUMBER: 09/588,947
;  PRIOR FILING DATE: 2000-06-08
;  PRIOR APPLICATION NUMBER: 09/507,968
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: 60/122,388
;  PRIOR FILING DATE: 1999-03-02
;  PRIOR APPLICATION NUMBER: 60/124,097
;  PRIOR FILING DATE: 1999-03-12
;  PRIOR APPLICATION NUMBER: 60/126,599
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: 60/127,598
;  PRIOR FILING DATE: 1999-04-02
;  PRIOR APPLICATION NUMBER: 60/130,412
;  PRIOR FILING DATE: 1999-04-16
;  PRIOR APPLICATION NUMBER: 60/130,696
;  PRIOR FILING DATE: 1999-04-23
;  PRIOR APPLICATION NUMBER: 60/131,278
;  PRIOR FILING DATE: 1999-04-27
;  PRIOR APPLICATION NUMBER: 60/131,673
;  PRIOR FILING DATE: 1999-04-29
;  PRIOR APPLICATION NUMBER: 60/136,784
;  PRIOR FILING DATE: 1999-05-28
;  PRIOR APPLICATION NUMBER: 60/142,659
;  PRIOR FILING DATE: 1999-07-06
;  PRIOR APPLICATION NUMBER: 60/145,824
;  PRIOR FILING DATE: 1999-07-27
;  PRIOR APPLICATION NUMBER: 60/167,239
;  PRIOR FILING DATE: 1999-11-24
;  PRIOR APPLICATION NUMBER: 60/168,624
;  PRIOR FILING DATE: 1999-12-03
;  PRIOR APPLICATION NUMBER: 60/171,108
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: 60/171,626
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: 60/176,015
;  PRIOR FILING DATE: 2000-01-14
;  PRIOR APPLICATION NUMBER: 09/255,794
;  PRIOR FILING DATE: 1999-02-23
;  PRIOR APPLICATION NUMBER: 09/005,874
;  PRIOR FILING DATE: 1998-01-12
;  PRIOR APPLICATION NUMBER: 60/036,100
;  PRIOR FILING DATE: 1997-01-14
;  PRIOR APPLICATION NUMBER: PCT/US96/17957
;  PRIOR FILING DATE: 1996-10-25
;  NUMBER OF SEQ ID NOS: 42
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;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
;   LENGTH: 266
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-588-947A-19

  Query Match             92.0%;  Score 1335.5;  DB 4;  Length 266;
  Best Local Similarity   93.3%;  Pred. No. 1.6e-146;
  Matches  266;  Conservative    0;  Mismatches    0;  Indels   19;  Gaps    1;

Qy          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60

Qy         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120

Qy        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
              ||||||||||||||||||||                    ||||||||||||||||||||
Db        121 GEGNSSQNSRNKRAVQGPEET------------------GSYTFVPWLLSFKRGSALEE 161

Qy        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 221

Qy        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
              |||||||||||||||||||||||||||||||||||||||||||||
Db        222 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 266


RESULT 10
US-09-589-287B-28
; Sequence 28, Application US/09589287B
; Patent No. 6403770
; GENERAL INFORMATION:
;  APPLICANT: Yu et al.
;  TITLE OF INVENTION: Antibodies to Neutrokine-alpha
;  FILE REFERENCE: PF343P3C1
;  CURRENT APPLICATION NUMBER: US/09/589,287B
;  CURRENT FILING DATE:  2000-06-08
;  Prior application data removed - check PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
;   LENGTH: 219
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-589-287B-28

  Query Match             74.4%;  Score 1080;  DB 4;  Length 219;
  Best Local Similarity   96.3%;  Pred. No. 5.5e-117;
  Matches  211;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         67 YQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAPGEGNSS 126
              |||||:||||||||||||||||||| | |||||| ||||||||||||||||||||||||
Db          1 YQVAAVQGDLASLRAELQGHHAEKLPARARAPKAGLGEAPAVTAGLKIFEPPAPGEGNSS 60

Qy        127 QNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEEKENKIL 186
              |:||||||:|| |||| ||||||||||||||||||||||||||||||||||||||||||
Db         61 QSSRNKRAIQGAEETVIQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEEKENKIL 120

Qy        187 VKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETLPNNSCY 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETLPNNSCY 180

Qy        247 SAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
              |||||||||||||||||||||||||||||||||||||||
Db        181 SAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 219


RESULT 11
US-09-588-947A-28
; Sequence 28, Application US/09588947A
; Patent No. 6562579
; GENERAL INFORMATION:
;  APPLICANT: Yu et al.
;  TITLE OF INVENTION: Diagnostic Methods Using Antibodies to Neutrokine-alpha
;  FILE REFERENCE: PF343P3C2
;  CURRENT APPLICATION NUMBER: US/09/588,947A
;  CURRENT FILING DATE:  2000-06-08
;  PRIOR APPLICATION NUMBER: 09/588,947
;  PRIOR FILING DATE: 2000-06-08
;  PRIOR APPLICATION NUMBER: 09/507,968
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: 60/122,388
;  PRIOR FILING DATE: 1999-03-02
;  PRIOR APPLICATION NUMBER: 60/124,097
;  PRIOR FILING DATE: 1999-03-12
;  PRIOR APPLICATION NUMBER: 60/126,599
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: 60/127,598
;  PRIOR FILING DATE: 1999-04-02
;  PRIOR APPLICATION NUMBER: 60/130,412
;  PRIOR FILING DATE: 1999-04-16
;  PRIOR APPLICATION NUMBER: 60/130,696
;  PRIOR FILING DATE: 1999-04-23
;  PRIOR APPLICATION NUMBER: 60/131,278
;  PRIOR FILING DATE: 1999-04-27
;  PRIOR APPLICATION NUMBER: 60/131,673
;  PRIOR FILING DATE: 1999-04-29
;  PRIOR APPLICATION NUMBER: 60/136,784
;  PRIOR FILING DATE: 1999-05-28
;  PRIOR APPLICATION NUMBER: 60/142,659
;  PRIOR FILING DATE: 1999-07-06
;  PRIOR APPLICATION NUMBER: 60/145,824
;  PRIOR FILING DATE: 1999-07-27
;  PRIOR APPLICATION NUMBER: 60/167,239
;  PRIOR FILING DATE: 1999-11-24
;  PRIOR APPLICATION NUMBER: 60/168,624
;  PRIOR FILING DATE: 1999-12-03
;  PRIOR APPLICATION NUMBER: 60/171,108
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: 60/171,626
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: 60/176,015
;  PRIOR FILING DATE: 2000-01-14
;  PRIOR APPLICATION NUMBER: 09/255,794
;  PRIOR FILING DATE: 1999-02-23
;  PRIOR APPLICATION NUMBER: 09/005,874
;  PRIOR FILING DATE: 1998-01-12
;  PRIOR APPLICATION NUMBER: 60/036,100
;  PRIOR FILING DATE: 1997-01-14
;  PRIOR APPLICATION NUMBER: PCT/US96/17957
;  PRIOR FILING DATE: 1996-10-25
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
;   LENGTH: 219
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-588-947A-28

  Query Match             74.4%;  Score 1080;  DB 4;  Length 219;
  Best Local Similarity   96.3%;  Pred. No. 5.5e-117;
  Matches  211;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         67 YQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAPGEGNSS 126
              |||||:||||||||||||||||||| | |||||| ||||||||||||||||||||||||
Db          1 YQVAAVQGDLASLRAELQGHHAEKLPARARAPKAGLGEAPAVTAGLKIFEPPAPGEGNSS 60

Qy        127 QNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEEKENKIL 186
              |:||||||:|| |||| ||||||||||||||||||||||||||||||||||||||||||
Db         61 QSSRNKRAIQGAEETVIQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEEKENKIL 120
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Qy        187 VKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETLPNNSCY 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETLPNNSCY 180

Qy        247 SAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
              |||||||||||||||||||||||||||||||||||||||
Db        181 SAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 219


RESULT 12
US-09-589-287B-30
; Sequence 30, Application US/09589287B
; Patent No. 6403770
; GENERAL INFORMATION:
;  APPLICANT: Yu et al.
;  TITLE OF INVENTION: Antibodies to Neutrokine-alpha
;  FILE REFERENCE: PF343P3C1
;  CURRENT APPLICATION NUMBER: US/09/589,287B
;  CURRENT FILING DATE:  2000-06-08
;  Prior application data removed - check PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
;   LENGTH: 219
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-589-287B-30

  Query Match             74.0%;  Score 1074;  DB 4;  Length 219;
  Best Local Similarity   95.9%;  Pred. No. 2.7e-116;
  Matches  210;  Conservative    3;  Mismatches    6;  Indels    0;  Gaps    0;

Qy         67 YQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAPGEGNSS 126
              |||||:|||||||||||| |||||||| | |||||| ||||||||||||||||||||||
Db          1 YQVAAVQGDLASLRAELQSHHAEKLPARARAPKAGLGEAPAVTAGLKIFEPPAPGEGNSS 60

Qy        127 QNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEEKENKIL 186
              |:|||||:|| |||| ||||||||||||||||||||||||||||||||||||||||||||
Db         61 QSSRNKRAIQGAEETVIQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEEKENKIL 120

Qy        187 VKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETLPNNSCY 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETLPNNSCY 180

Qy        247 SAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
              |||||||||||||||||||||||||||||||||||||||
Db        181 SAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 219


RESULT 13
US-09-588-947A-30
; Sequence 30, Application US/09588947A
; Patent No. 6562579
; GENERAL INFORMATION:
;  APPLICANT: Yu et al.
;  TITLE OF INVENTION: Diagnostic Methods Using Antibodies to Neutrokine-alpha
;  FILE REFERENCE: PF343P3C2
;  CURRENT APPLICATION NUMBER: US/09/588,947A
;  CURRENT FILING DATE:  2000-06-08
;  PRIOR APPLICATION NUMBER: 09/588,947
;  PRIOR FILING DATE: 2000-06-08
;  PRIOR APPLICATION NUMBER: 09/507,968
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: 60/122,388
;  PRIOR FILING DATE: 1999-03-02
;  PRIOR APPLICATION NUMBER: 60/124,097
;  PRIOR FILING DATE: 1999-03-12
;  PRIOR APPLICATION NUMBER: 60/126,599
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: 60/127,598
;  PRIOR FILING DATE: 1999-04-02
;  PRIOR APPLICATION NUMBER: 60/130,412
;  PRIOR FILING DATE: 1999-04-16
;  PRIOR APPLICATION NUMBER: 60/130,696
;  PRIOR FILING DATE: 1999-04-23
;  PRIOR APPLICATION NUMBER: 60/131,278
;  PRIOR FILING DATE: 1999-04-27
;  PRIOR APPLICATION NUMBER: 60/131,673
;  PRIOR FILING DATE: 1999-04-29
;  PRIOR APPLICATION NUMBER: 60/136,784
;  PRIOR FILING DATE: 1999-05-28
;  PRIOR APPLICATION NUMBER: 60/142,659
;  PRIOR FILING DATE: 1999-07-06
;  PRIOR APPLICATION NUMBER: 60/145,824
;  PRIOR FILING DATE: 1999-07-27
;  PRIOR APPLICATION NUMBER: 60/167,239
;  PRIOR FILING DATE: 1999-11-24
;  PRIOR APPLICATION NUMBER: 60/168,624
;  PRIOR FILING DATE: 1999-12-03
;  PRIOR APPLICATION NUMBER: 60/171,108
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: 60/171,626
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: 60/176,015
;  PRIOR FILING DATE: 2000-01-14
;  PRIOR APPLICATION NUMBER: 09/255,794
;  PRIOR FILING DATE: 1999-02-23
;  PRIOR APPLICATION NUMBER: 09/005,874
;  PRIOR FILING DATE: 1998-01-12
;  PRIOR APPLICATION NUMBER: 60/036,100
;  PRIOR FILING DATE: 1997-01-14
;  PRIOR APPLICATION NUMBER: PCT/US96/17957
;  PRIOR FILING DATE: 1996-10-25
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
;   LENGTH: 219
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-588-947A-30

  Query Match             74.0%;  Score 1074;  DB 4;  Length 219;
  Best Local Similarity   95.9%;  Pred. No. 2.7e-116;
  Matches  210;  Conservative    3;  Mismatches    6;  Indels    0;  Gaps    0;

Qy         67 YQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAPGEGNSS 126
              |||||:|||||||||||| |||||||| | |||||| ||||||||||||||||||||||
Db          1 YQVAAVQGDLASLRAELQSHHAEKLPARARAPKAGLGEAPAVTAGLKIFEPPAPGEGNSS 60

Qy        127 QNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEEKENKIL 186
              |:|||||:|| |||| ||||||||||||||||||||||||||||||||||||||||||||
Db         61 QSSRNKRAIQGAEETVIQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEEKENKIL 120

Qy        187 VKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETLPNNSCY 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETLPNNSCY 180

Qy        247 SAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
              |||||||||||||||||||||||||||||||||||||||
Db        181 SAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 219


RESULT 14
US-09-496-118B-5
; Sequence 5, Application US/09496118B
; Patent No. 6475986
; GENERAL INFORMATION:
;  APPLICANT:  Aggarwal, Bharat B.
;  TITLE OF INVENTION:  Uses of THANK, a TNF homologue that Activates
;  TITLE OF INVENTION:  Apoptosis
;  FILE REFERENCE:  D6206
;  CURRENT APPLICATION NUMBER: US/09/496,118B
;  CURRENT FILING DATE:  2000-02-01
;  PRIOR APPLICATION NUMBER:  US 60/118,531
;  PRIOR FILING DATE:  1999-02-02
;  NUMBER OF SEQ ID NOS:  13
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; SEQ ID NO 5
;   LENGTH: 174
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: domain
;   LOCATION: 112..285
;   OTHER INFORMATION: sequence of THANK extracellular domain
US-09-496-118B-5

  Query Match            62.1%;  Score 901;  DB 4;  Length 174;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-96;
  Matches  174;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        112 LKIFEPPAPGEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLS 171
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 LKIFEPPAPGEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLS 60

Qy        172 FKRGSALEEKENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFR 231
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FKRGSALEEKENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFR 120

Qy        232 CIQNMPETLPNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
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RESULT 15
US-09-589-287B-38
; Sequence 38, Application US/09589287B
; Patent No. 6403770
; GENERAL INFORMATION:
;  APPLICANT: Yu et al.
;  TITLE OF INVENTION: Antibodies to Neutrokine-alpha
;  FILE REFERENCE: PF343P3C1
;  CURRENT APPLICATION NUMBER: US/09/589,287B
;  CURRENT FILING DATE:  2000-06-08
;  Prior application data removed - check PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
;   LENGTH: 289
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-589-287B-38

  Query Match            54.7%;  Score 793;  DB 4;  Length 289;
  Best Local Similarity  55.0%;  Pred. No. 1.8e-83;
  Matches  175;  Conservative   30;  Mismatches   51;  Indels   62;  Gaps    6;

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Qy        268 AQISLDGDVTFFGALKLL 285
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Job time : 19 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 28, 2003, 18:05:47 ; Search time 60 Seconds
(without alignments)
649.714 Million cell updates/sec

Title: US-09-507-968D-2
Perfect score: 1451
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 510680 seqs, 136781880 residues

Total number of hits satisfying chosen parameters: 510680

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1451	100.0	285	9	US-09-193-663-2	Sequence 2, Appli
3	1451	100.0	285	9	US-09-877-156-1	Sequence 1, Appli
4	1451	100.0	285	9	US-09-879-919-23	Sequence 23, Appl
5	1451	100.0	285	10	US-09-929-493-2	Sequence 2, Appli
6	1451	100.0	285	10	US-09-779-050A-2	Sequence 2, Appli
7	1451	100.0	285	11	US-09-302-863-4	Sequence 4, Appli
8	1451	100.0	285	11	US-09-880-748-3228	Sequence 3228, Ap
9	1451	100.0	285	11	US-09-932-613-173	Sequence 173, App
10	1451	100.0	285	12	US-10-137-870-24	Sequence 24, Appl
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12	1451	100.0	285	12	US-10-140-021-24	Sequence 24, Appl
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16	1451	100.0	285	12	US-10-140-922-24	Sequence 24, Appl
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19	1451	100.0	285	12	US-10-141-698-24	Sequence 24, Appl
20	1451	100.0	285	12	US-10-141-702-24	Sequence 24, Appl
21	1451	100.0	285	12	US-10-141-704-24	Sequence 24, Appl
22	1451	100.0	285	12	US-10-142-421-24	Sequence 24, Appl
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29	1451	100.0	285	12	US-10-145-633-24	Sequence 24, Appl
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31	1451	100.0	285	12	US-10-145-748-24	Sequence 24, Appl
32	1451	100.0	285	12	US-10-145-823-24	Sequence 24, Appl
33	1451	100.0	285	12	US-10-145-826-24	Sequence 24, Appl
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40	1451	100.0	285	12	US-10-147-495-24	Sequence 24, Appl
41	1451	100.0	285	12	US-10-147-501-24	Sequence 24, Appl
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45	1451	100.0	285	12	US-10-147-510-24	Sequence 24, Appl

ALIGNMENTS

P3330R1C37D

RESULT 1
US-08-971-317A-2
; Sequence 2, Application US/08971317A
; Publication No. US20010010925A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971,317A
; FILING DATE: 17-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Goller, Mimi C
; REGISTRATION NUMBER: 39,046
; REFERENCE/DOCKET NUMBER: 6255.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (847) 935-7550
; TELEFAX: (847) 938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

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;      LENGTH:  285 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  No. US20010010925A1e
US-08-971-317A-2

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  Best Local Similarity   100.0%;  Pred. No. 2.9e-139;
  Matches  285;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
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Qy        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
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RESULT 2
US-09-193-663-2
; Sequence 2, Application US/09193663
; Patent No. US20020055624A1
; GENERAL INFORMATION:
;  APPLICANT: Wiley, Steven R.
;  TITLE OF INVENTION: TNF-DELTA LIGAND AND USES THEREOF
;  FILE REFERENCE: 6255.US.02
;  CURRENT APPLICATION NUMBER: US/09/193,663
;  CURRENT FILING DATE: 1998-11-17
;  EARLIER APPLICATION NUMBER: 60/065,916
;  EARLIER FILING DATE: 1997-11-17
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 285
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-193-663-2

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Db        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285


RESULT 3
US-09-877-156-1
; Sequence 1, Application US/09877156
; Patent No. US20020055625A1
; GENERAL INFORMATION:
;  APPLICANT: Catherine Tribouley
;  TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
;  FILE REFERENCE: 1408.003/200130.439C1
;  CURRENT APPLICATION NUMBER: US/09/877,156
;  CURRENT FILING DATE:  2001-06-08
;  PRIOR APPLICATION NUMBER: US 09/286,529
;  PRIOR FILING DATE: 1998-04-05
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
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;   TYPE: PRT
;   ORGANISM: human
US-09-877-156-1

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; Patent No. US20020064829A1
; GENERAL INFORMATION:
;  APPLICANT: Yu, Guo-Liang, et al.
;  TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
;  FILE REFERENCE: PF253P1
;  CURRENT APPLICATION NUMBER: US/09/879,919
;  CURRENT FILING DATE:  2001-06-14
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,978
;  PRIOR FILING DATE: 2001-03-23
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/254,875
;  PRIOR FILING DATE: 2000-12-13
;  PRIOR APPLICATION NUMBER: 60/241,952
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/211,537
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 08/815,783
;  PRIOR FILING DATE: 1997-03-12
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;  PRIOR APPLICATION NUMBER: 60/016,812
;  PRIOR FILING DATE: 1996-03-14
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
;   LENGTH: 285
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-879-919-23

  Query Match            100.0%;  Score 1451;  DB 9;  Length 285;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-139;
  Matches  285;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60
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Qy         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120
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Qy        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
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Qy        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240
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RESULT 5
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; Sequence 2, Application US/09929493
; Patent No. US20020115112A1
; GENERAL INFORMATION:
;  APPLICANT: Yu et al.
;  TITLE OF INVENTION: Neutrokine-alpha and Neutrokine-alpha Splice Variant
;  FILE REFERENCE: PF343P4
;  CURRENT APPLICATION NUMBER: US/09/929,493
;  CURRENT FILING DATE:  2001-08-15
;  PRIOR APPLICATION NUMBER: 60/225,628
;  PRIOR FILING DATE: 2000-08-15
;  PRIOR APPLICATION NUMBER: 60/227,008
;  PRIOR FILING DATE: 2000-08-23
;  PRIOR APPLICATION NUMBER: 60/234,338
;  PRIOR FILING DATE: 2000-09-22
;  PRIOR APPLICATION NUMBER: 60/240,806
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/250,020
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-06
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/296,122
;  PRIOR FILING DATE: 2001-06-07
;  PRIOR APPLICATION NUMBER: 60/304,809
;  PRIOR FILING DATE: 2001-07-13
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 285
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-929-493-2

  Query Match            100.0%;  Score 1451;  DB 10;  Length 285;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-139;
  Matches  285;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60
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Qy        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
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Qy        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240

Qy        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
              |||||||||||||||||||||||||||||||||||||||||||||
Db        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285


RESULT 6
US-09-779-050A-2
; Sequence 2, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
;  APPLICANT: BOYLE, WILLIAM
;  APPLICANT:  HSU, HAILING
;  TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
;  FILE REFERENCE: A-570B
;  CURRENT APPLICATION NUMBER: US/09/779,050A
;  CURRENT FILING DATE:  2001-02-12
;  PRIOR APPLICATION NUMBER: 60/181,800
;  PRIOR FILING DATE: 2000-02-11
;  NUMBER OF SEQ ID NOS: 52
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 285
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-779-050A-2

  Query Match            100.0%;  Score 1451;  DB 10;  Length 285;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-139;
  Matches  285;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60

Qy         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120

Qy        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180

Qy        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240

Qy        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
              |||||||||||||||||||||||||||||||||||||||||||||
Db        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285


RESULT 7
US-09-302-863-4
; Sequence 4, Application US/09302863
; Publication No. US20030022233A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: Goodwin, Raymond G
;  APPLICANT: Din, Wanwan S.
;  TITLE OF INVENTION: METHODS OF USE OF THE TACI/TACI-L INTERACTION
;  FILE REFERENCE: 2519
;  CURRENT APPLICATION NUMBER: US/09/302,863
;  CURRENT FILING DATE: 1999-04-30
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 285
;   TYPE: PRT
;   ORGANISM: Human
US-09-302-863-4

  Query Match            100.0%;  Score 1451;  DB 11;  Length 285;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-139;
  Matches  285;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60

Qy         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120

Qy        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180

Qy        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240

Qy        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
              |||||||||||||||||||||||||||||||||||||||||||||
Db        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285


RESULT 8
US-09-880-748-3228
; Sequence 3228, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523
;  CURRENT APPLICATION NUMBER: US/09/880,748
;  CURRENT FILING DATE:  2001-06-15
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 3239
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3228
;   LENGTH: 285
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-880-748-3228

  Query Match            100.0%;  Score 1451;  DB 11;  Length 285;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-139;
  Matches  285;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60

Qy         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120

Qy        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180

Qy        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240

Qy        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
              |||||||||||||||||||||||||||||||||||||||||||||
Db        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285


RESULT 9
US-09-932-613-173
; Sequence 173, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  APPLICANT:  Beltzer, James P.
;  APPLICANT:  Potter, M. Daniel
;  APPLICANT:  Fleming, Tony J.
;  APPLICANT:  Rosen, Craig A.
;  TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
;  FILE REFERENCE: Dyx-025.1 PCT; DYX-025.1 US
;  CURRENT APPLICATION NUMBER: US/09/932,613
;  CURRENT FILING DATE:  2001-08-17
;  NUMBER OF SEQ ID NOS: 458
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 173
;   LENGTH: 285
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-09-932-613-173

  Query Match            100.0%;  Score 1451;  DB 11;  Length 285;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-139;
  Matches  285;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60

Qy         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120

Qy        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180

Qy        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240

Qy        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
              |||||||||||||||||||||||||||||||||||||||||||||
Db        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285


RESULT 10
US-10-137-870-24
; Sequence 24, Application US/10137870
; Publication No. US20030138883A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
```

```
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C155
;  CURRENT APPLICATION NUMBER: US/10/137,870
;  CURRENT FILING DATE:  2002-05-03
;  Prior Application removed - See Palm or File Wrapper
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 24
;   LENGTH: 285
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-137-870-24

  Query Match            100.0%;  Score 1451;  DB 12;  Length 285;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-139;
  Matches  285;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60

Qy         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120

Qy        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180

Qy        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240

Qy        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
              |||||||||||||||||||||||||||||||||||||||||||||
Db        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285


RESULT 11
US-10-140-018-24
; Sequence 24, Application US/10140018
; Publication No. US20030138885A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C158
;  CURRENT APPLICATION NUMBER: US/10/140,018
;  CURRENT FILING DATE:  2002-05-06
;  Prior Application removed - See Palm or File Wrapper
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 24
;   LENGTH: 285
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-140-018-24

  Query Match            100.0%;  Score 1451;  DB 12;  Length 285;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-139;
  Matches  285;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60

Qy         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120

Qy        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180

Qy        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240

Qy        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
              |||||||||||||||||||||||||||||||||||||||||||||
Db        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285


RESULT 12
US-10-140-021-24
; Sequence 24, Application US/10140021
; Publication No. US20030138886A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C167
;  CURRENT APPLICATION NUMBER: US/10/140,021
;  CURRENT FILING DATE:  2002-05-06
;  Prior Application removed - See Palm or File Wrapper
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 24
;   LENGTH: 285
;   TYPE: PRT
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;   ORGANISM: Homo Sapien
US-10-140-021-24

  Query Match           100.0%;  Score 1451;  DB 12;  Length 285;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-139;
  Matches  285;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60

Qy         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120

Qy        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180

Qy        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240

Qy        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
              |||||||||||||||||||||||||||||||||||||||||||||
Db        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285


RESULT 13
US-10-140-274-24
; Sequence 24, Application US/10140274
; Publication No. US20030143674A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C161
;  CURRENT APPLICATION NUMBER: US/10/140,274
;  CURRENT FILING DATE:  2002-05-06
;  Prior Apploication removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 24
;   LENGTH: 285
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-140-274-24

  Query Match           100.0%;  Score 1451;  DB 12;  Length 285;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-139;
  Matches  285;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60

Qy         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120

Qy        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180

Qy        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240

Qy        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
              |||||||||||||||||||||||||||||||||||||||||||||
Db        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285


RESULT 14
US-10-140-471-24
; Sequence 24, Application US/10140471
; Publication No. US20030138887A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C163
;  CURRENT APPLICATION NUMBER: US/10/140,471
;  CURRENT FILING DATE:  2002-05-06
;  Prior Apploication removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 24
;   LENGTH: 285
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-140-471-24

  Query Match           100.0%;  Score 1451;  DB 12;  Length 285;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-139;
  Matches  285;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60
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Db          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60

Qy         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120

Qy        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
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Db        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180

Qy        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240
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Db        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240

Qy        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
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Db        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
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RESULT 15
US-10-140-807-24
; Sequence 24, Application US/10140807
; Publication No. US20030134354A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C174
;  CURRENT APPLICATION NUMBER: US/10/140,807
;  CURRENT FILING DATE:  2002-05-07
;  Prior Apploication removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 24
;   LENGTH: 285
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-140-807-24

  Query Match             100.0%;  Score 1451;  DB 12;  Length 285;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-139;
  Matches  285;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60

Qy         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120

Qy        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180

Qy        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240

Qy        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
              |||||||||||||||||||||||||||||||||||||||||||||
Db        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285


Search completed: August 28, 2003, 18:14:54
Job time : 61 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 28, 2003, 17:59:46 ; Search time 23 Seconds
(without alignments)
582.722 Million cell updates/sec

Title: US-09-507-968D-2
Perfect score: 1451
Sequence: 1 MDDSTEREQSRLTSCLKKRE.....ENAQISLDGDVTFFGALKLL 285

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1451	100.0	285	1	T13B_HUMAN	Q9y275 homo sapien
2	910	62.7	309	1	T13B_MOUSE	Q9wu72 mus musculu
3	246.5	17.0	241	1	TN13_MOUSE	Q9d777 mus musculu
4	244.5	16.9	250	1	TN13_HUMAN	O75888 homo sapien
5	118.5	8.2	233	1	TNFA_CANFA	P51742 canis famil
6	116.5	8.0	233	1	TNFA_TURTR	Q9bea1 tursiops tr
7	111.5	7.7	233	1	TNFA_FELCA	P19101 felis silve
8	110.5	7.6	233	1	TNFA_DELLE	Q8wnr1 delphinapte
9	110.5	7.6	235	1	TNFA_RAT	P16599 rattus norv
10	109.5	7.5	235	1	TNFA_MOUSE	P06804 mus musculu
11	108	7.4	233	1	TNFA_BOVIN	Q06599 bos taurus
12	107.5	7.4	235	1	TNFA_PERLE	P36939 peromyscus
13	107	7.4	232	1	TNFA_PIG	P23563 sus scrofa
14	106.5	7.3	234	1	TNFA_CAPHI	P13296 capra hircu
15	105.5	7.3	233	1	TNFA_LAMGL	P59694 lama glama
16	104	7.2	232	1	TNFA_PANTR	Q8hzd9 pan troglod
17	103.5	7.1	234	1	TNFA_BOSIN	P59684 bos indicus
18	103	7.1	233	1	TNFA_BUBBU	P59693 bubalus bub
19	103	7.1	391	1	EDA_BOVIN	Q9beg5 bos taurus
20	102.5	7.1	234	1	TNFA_SHEEP	P23383 ovis aries
21	102.5	7.1	391	1	EDA_HUMAN	Q92838 homo sapien
22	102.5	7.1	391	1	EDA_MOUSE	O54693 mus musculu
23	101.5	7.0	229	1	TNFA_CEREL	P51743 cervus elap
24	100.5	6.9	205	1	TNFB_HUMAN	P01374 homo sapien
25	99	6.8	234	1	TNFA_CAVPO	P51435 cavia porce
26	98.5	6.8	233	1	TNFA_HUMAN	P01375 homo sapien
27	97.5	6.7	184	1	YGFB_PSEAE	Q9htw5 pseudomonas
28	97.5	6.7	281	1	TNF6_HUMAN	P48023 homo sapien
29	97	6.7	281	1	TN10_HUMAN	P50591 homo sapien
30	95.5	6.6	233	1	TNFA_SAISC	Q8mkg8 saimiri sci
31	95.5	6.6	280	1	TNF6_MACMU	Q9myl6 macaca mula
32	95	6.5	233	1	TNFA_TRIVU	P79374 trichosurus
33	93.5	6.4	235	1	TNFA_RABIT	P04924 oryctolagus
34	93.5	6.4	282	1	TNF6_PIG	Q9bea8 sus scrofa
35	93.5	6.4	651	1	E2BD_YEAST	P12754 saccharomyc
36	92.5	6.4	253	1	TNFA_SPAAU	Q8jfg3 sparus aura
37	92.5	6.4	280	1	TNF6_CERTO	Q9bdn1 cercocebus
38	90.5	6.2	204	1	TNFB_PIG	P26445 sus scrofa
39	89.5	6.2	233	1	TNFA_PAPSP	P33620 papio sp. (
40	89.5	6.2	234	1	TNFA_HORSE	P29553 equus cabal
41	89	6.1	1267	1	HMT1_HUMAN	Q9h9b1 homo sapien
42	87.5	6.0	233	1	TNFA_PAPAN	P59695 papio anubi
43	87.5	6.0	233	1	TNFA_PAPHU	O77510 papio hamad
44	87.5	6.0	993	1	TSH_DROME	P22265 drosophila
45	86.5	6.0	233	1	TNFA_MARMO	O35734 marmota mon

ALIGNMENTS

RESULT 1
T13B_HUMAN
ID T13B_HUMAN STANDARD; PRT; 285 AA.
AC Q9Y275;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 13B (TNF-and APOL-
DE related leukocyte expressed ligand 1) (TALL-1) (B lymphocyte
DE stimulator) (BLyS) (B cell-activating factor) (BAFF) (Dendritic cell-
DE derived TNF-like molecule).
GN TNFSF13B OR TALL1 OR BLYS OR BAFF OR ZTNF4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99260341; PubMed=10331498;
RA Shu H.-B., Hu W.-H., Johnson H.;
RT "TALL-1 is a novel member of the TNF family that is down-regulated by
RT mitogens.";
RL J. Leukoc. Biol. 65:680-683(1999).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 134-148.
RX MEDLINE=99288033; PubMed=10359578;
RA Schneider P., MacKay F., Steiner V., Hofmann K., Bodmer J.-L.,
RA Holler N., Ambrose C., Lawton P., Bixler S., Acha-Orbea H.,
RA Valmori D., Romero P., Werner-Favre C., Zubler R.H., Browning J.L.,
RA Tschopp J.;
RT "BAFF, a novel ligand of the tumor necrosis factor family, stimulates
RT B cell growth.";
RL J. Exp. Med. 189:1747-1756(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Monocytes, and Neutrophils;
RX MEDLINE=99329343; PubMed=10398604;
RA Moore P.A., Belvedere O., Orr A., Pieri K., LaFleur D.W., Feng P.,
RA Soppet D., Charters M., Gentz R., Parmelee D., Li Y., Galperina O.,
RA Giri J., Roschke V., Nardelli B., Carrell J., Sosnovtseva S.,
RA Greenfield W., Ruben S.M., Olsen H.S., Fikes J., Hilbert D.M.;
RT "BLyS: member of the tumor necrosis factor family and B lymphocyte
RT stimulator.";
RL Science 285:260-263(1999).
RN [4]
RP SEQUENCE FROM N.A.
RA Farrah T., Gross J., Piddington C., O'Hara P.;
RT "Homo sapiens homolog of tumor necrosis factor.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Dendritic cell;
RA Zhang W., Wan T., Yu Y., Cao X.;
RT "A novel dendritic cell-derived TNF-like molecule.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
RN [6]

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RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [7]
RP   SEQUENCE OF 1-135 FROM N.A., AND VARIANT THR-105.
RA   Kawasaki A., Tsuchiya N., Fukazawa T., Hashimoto H., Tokunaga K.;
RT   "New polymorphisms of human BLyS gene.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
RN   [8]
RP   FUNCTION.
RX   MEDLINE=21170294; PubMed=10973284;
RA   Yu G., Boone T., Delaney J., Hawkins N., Kelley M.J., Ramakrishnan M.,
RA   McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
RA   Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.;
RT   "APRIL and TALL-I and receptors BCMA and TACI: system for regulating
RT   humoral immunity.";
RL   Nat. Immunol. 1:252-256(2000).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 142-285.
RX   MEDLINE=21842897; PubMed=11853672;
RA   Liu Y., Xu L., Opalka N., Kappler J., Shu H.-B., Zhang G.;
RT   "Crystal structure of sTALL-1 reveals a virus-like assembly of TNF
RT   family ligands.";
RL   Cell 108:383-394(2002).
RN   [10]
RP   X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 136-285.
RX   MEDLINE=21686304; PubMed=11827482;
RA   Karpusas M., Cachero T.G., Qian F., Boriack-Sjodin A., Mullen C.,
RA   Strauch K., Hsu Y.-M., Kalled S.L.;
RT   "Crystal structure of extracellular human BAFF, a TNF family member
RT   that stimulates B lymphocytes.";
RL   J. Mol. Biol. 315:1145-1154(2002).
RN   [11]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 134-285.
RX   MEDLINE=21912420; PubMed=11862220;
RA   Oren D.A., Li Y., Volovik Y., Morris T.S., Dharia C., Das K.,
RA   Galperina O., Gentz R., Arnold E.;
RT   "Structural basis of BLyS receptor recognition.";
RL   Nat. Struct. Biol. 9:288-292(2002).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF13B/TACI and TNFRSF17/BCMA.
CC       TNFSF13/APRIL binds to the same 2 receptors. Together, they form a
CC       2 ligands -2 receptors pathway involved in the stimulation of B-
CC       and T-cell function and the regulation of humoral immunity. A
CC       third B-cell specific BAFF-receptor (BAFFR/BR3) promotes the
CC       survival of mature B-cells and the B-cell response.
CC   -!- SUBUNIT: Homotrimer.
CC   -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC       EXTRACELLULAR SOLUBLE FORM.
CC   -!- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN PERIPHERAL BLOOD
CC       LEUKOCYTES AND IS SPECIFICALLY EXPRESSED IN MONOCYTES AND
CC       MACROPHAGES. ALSO FOUND IN THE SPLEEN, LYMPH NODE, BONE MARROW, T-
CC       CELLS AND DENDRITIC CELLS. A LOWER EXPRESSION SEEN IN PLACENTA,
CC       HEART, LUNG, FETAL LIVER, THYMUS, AND PANCREAS.
CC   -!- INDUCTION: UPREGULATED BY EXPOSURE TO INTERFERON-GAMMA. DOWN-
CC       REGULATED BY PHORBOL MYRISTATE ACETATE/IONOMYCIN TREATMENT.
CC   -!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC       PROTEOLYTIC PROCESSING.
CC   -!- PTM: N-glycosylated.
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF136293; AAD29421.1; -.
DR   EMBL; AF116456; AAD25356.1; -.
DR   EMBL; AF132600; AAD21092.1; -.
DR   EMBL; AF186114; AAF01432.1; -.
DR   EMBL; AF134715; AAF60219.1; -.
DR   EMBL; AB073225; BAB90856.1; -.
DR   EMBL; BC020674; AAH20674.1; -.
DR   PDB; 1KXG; 03-APR-02.
DR   PDB; 1KD7; 12-NOV-02.
DR   PDB; 1JH5; 08-FEB-02.
DR   Genew; HGNC:11929; TNFSF13B.
DR   MIM; 603969; -.
DR   GO; GO:0005625; C:soluble fraction; TAS.
DR   GO; GO:0008283; P:cell proliferation; TAS.
DR   GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR006052; TNF_family.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; FALSE_NEG.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Transmembrane; Glycoprotein; Signal-anchor; 3D-structure;
KW   Polymorphism.
FT   CHAIN         1    285       TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT                                MEMBER 13B, MEMBRANE FORM.
FT   CHAIN       134    285       TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT                                MEMBER 13B, SOLUBLE FORM.
FT   DOMAIN        1     46       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     47     67       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN       68    285       EXTRACELLULAR (POTENTIAL).
FT   SITE        133    134       CLEAVAGE.
FT   DISULFID    232    245
FT   CARBOHYD    124    124       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    242    242       N-LINKED (GLCNAC. . .) (HIGH MANNOSE).
FT   VARIANT     105    105       A -> T.
FT                                /FTId=VAR_013483.
FT   STRAND      146    151
FT   TURN        153    154
FT   STRAND      158    160
FT   TURN        161    162
FT   STRAND      163    165
FT   STRAND      168    174
FT   STRAND      178    181
FT   TURN        182    183
FT   STRAND      184    187
FT   STRAND      191    201
FT   STRAND      208    215
FT   TURN        221    222
FT   STRAND      226    234
FT   STRAND      243    253
FT   TURN        255    256
FT   STRAND      258    263
FT   TURN        266    267
FT   STRAND      270    270
FT   TURN        274    276
FT   STRAND      278    283
SQ   SEQUENCE   285 AA;  31222 MW;  48ED0D7AB38C8867 CRC64;
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  Query Match           100.0%;  Score 1451;  DB 1;  Length 285;
  Best Local Similarity  100.0%;  Pred. No. 1.9e-116;
  Matches  285;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60

Qy         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120

Qy        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180

Qy        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240

Qy        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
              |||||||||||||||||||||||||||||||||||||||||||||
Db        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285


RESULT 2
T13B_MOUSE
ID   T13B_MOUSE     STANDARD;      PRT;   309 AA.
AC   Q9WU72;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor ligand superfamily member 13B (B cell-activating
DE   factor) (BAFF).
GN   TNFSF13B OR BAFF.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99288033; PubMed=10359578;
RA   Schneider P., MacKay F., Steiner V., Hofmann K., Bodmer J.-L.,
RA   Holler N., Ambrose C., Lawton P., Bixler S., Acha-Orbea H.,
RA   Valmori D., Romero P., Werner-Favre C., Zubler R.H., Browning J.L.,
RA   Tschopp J.;
RT   "BAFF, a novel ligand of the tumor necrosis factor family, stimulates
RT   B cell growth.";
RL   J. Exp. Med. 189:1747-1756(1999).
RN   [2]
RP   SEQUENCE FROM N.A., AND VARIANT SER-79.
RC   STRAIN=NZB;
RX   MEDLINE=21850530; PubMed=11862414;
RA   Jiang Y., Ohtsuji M., Abe M., Li N., Xiu Y., Wen X.S., Shirai T.,
RA   Hirose S.;
RT   "Polymorphism and chromosomal mapping of the mouse gene for B-cell
RT   activating factor belonging to the tumor necrosis factor family
RT   (Baff) and association with the autoimmune phenotype.";
RL   Immunogenetics 53:810-813(2001).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF13B/TACI and TNFRSF17/BCMA.
CC       TNFSF13/APRIL binds to the same 2 receptors. Together, they form a
CC       2 ligands -2 receptors pathway involved in the stimulation of B-
CC       and T-cell function and the regulation of humoral immunity. A
CC       third B-cell specific BAFF-receptor (BAFFR/BR3) promotes the
CC       survival of mature B-cells and the B-cell response.
CC   -!- SUBUNIT: Homotrimer.
CC   -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC       EXTRACELLULAR SOLUBLE FORM.
CC   -!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC       PROTEOLYTIC PROCESSING.
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF119383; AAD22475.1; -.
DR   EMBL; AF352245; AAL83939.1; -.
DR   MGD; MGI:1344376; Tnfsf13b.
DR   InterPro; IPR006052; TNF_family.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; FALSE_NEG.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Transmembrane; Glycoprotein; Signal-anchor;
KW   Polymorphism.
FT   CHAIN         1    309       TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT                                MEMBER 13B, MEMBRANE FORM.
FT   CHAIN       127    309       TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT                                MEMBER 13B, SOLUBLE FORM.
FT   DOMAIN        1     47       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     48     68       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN       69    309       EXTRACELLULAR (POTENTIAL).
FT   SITE        126    127       CLEAVAGE (BY SIMILARITY).
FT   DISULFID    256    269       BY SIMILARITY.
FT   CARBOHYD    117    117       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    266    266       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT      79     79       N -> S (IN STRAIN NZB).
SQ   SEQUENCE   309 AA;  34192 MW;  F3DE6056E66034B4 CRC64;

  Query Match           62.7%;  Score 910;  DB 1;  Length 309;
  Best Local Similarity  60.4%;  Pred. No. 2.8e-70;
  Matches  192;  Conservative   33;  Mismatches   51;  Indels   42;  Gaps    5;

Qy          1 MDDSTER-EQSRLTSCLKKREEMKLKECVSILPRKESPS-VRSSKDGKLLAATLLLALLS 58
              ||:| :      |  | :| |:||:     | |:||  :     :||:|||||||||||||
Db          1 MDESAKTLPPPCLCFCSEKGEDMKV-GYDPITPQKEEGAWFGICRDGRLLAATLLLALLS 59

Qy         59 CCLTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPP 118
               | :| ||:|||| || :|| ||| :     || ||||:        :|||:|:  |
Db         60 SSFTAMSLYQLAALQADLMNLRMELQSYRGSATPAAAGAPE--------LTAGVKLLTPA 111

Qy        119 APGEGNSSQNSRNKRAVQGPEET-----------------------------VTQDCL 147
              ||   |||:  ||:|| ||||||                             : ||||
Db        112 APRPHNSSRGHRNRRAFQGPEETEQDVDLSAPPAPCLPGCRHSQHDDNGMNLRNIIQDCL 171

Qy        148 QLIADSETPTIQKGSYTFVPWLLSFKRGSALEEKENKILVKETGYFFIYGQVLYTDKTYA 207
              ||||||:||||:||:|||||||||||||:|||||||||:|::||||||| |||||  :|
Db        172 QLIADSDTPTIRKGTYTFVPWLLSFKRGNALEEKENKIVVRQTGYFFIYSQVLYTDPIFA 231

Qy        208 MGHLIQRKKVHVFGDELSLVTLFRCIQNMPETLPNNSCYSAGIAKLEEGDELQLAIPREN 267
              |||:|||||||||||||||||||||||||:||||||||||||||:||||||:||||||||
Db        232 MGHVIQRKKVHVFGDELSLVTLFRCIQNMPKTLPNNSCYSAGIARLEEGDEIQLAIPREN 291

Qy        268 AQISLDGDVTFFGALKLL 285
              |||| :|| |||||||||
Db        292 AQISRNGDDTFFGALKLL 309


RESULT 3
TN13_MOUSE
ID   TN13_MOUSE     STANDARD;      PRT;   241 AA.
AC   Q9D777; Q9ERP1;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor ligand superfamily member 13 (A proliferation-
DE   inducing ligand) (APRIL).
GN   TNFSF13 OR APRIL.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=21170294; PubMed=10973284;
RA   Yu G., Boone T., Delaney J., Hawkins N., Kelley M.J., Ramakrishnan M.,
RA   McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
RA   Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.;
RT   "APRIL and TALL-I and receptors BCMA and TACI: system for regulating
RT   humoral immunity.";
RL   Nat. Immunol. 1:252-256(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Tongue;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF13B/TACI and to
CC       TNFRSF17/BCMA. May be implicated in the regulation of tumor cell
CC       growth. May be involved in monocyte/macrophage-mediated
CC       immunological processes.
CC   -!- SUBUNIT: Homotrimer (Potential).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing.
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF294825; AAG22534.1; -.
DR   EMBL; AK009514; BAB26332.1; -.
DR   MGD; MGI:1916833; Tnfsf13.
DR   GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
DR   InterPro; IPR006052; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Immune response; Glycoprotein.
FT   PROPEP          1     95       BY SIMILARITY.
FT   CHAIN          96    241       TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT                                   MEMBER 13.
FT   SITE           95     96       CLEAVAGE (BY FURIN) (BY SIMILARITY).
FT   DISULFID      187    202       POTENTIAL.
FT   CARBOHYD      115    115       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT      120    120       MISSING (IN REF. 2).
SQ   SEQUENCE   241 AA;  26889 MW;  4B96D03BDBC712A4 CRC64;

  Query Match             17.0%;  Score 246.5;  DB 1;  Length 241;
  Best Local Similarity   30.1%;  Pred. No. 7.7e-14;
  Matches   75;  Conservative   40;  Mismatches   81;  Indels   53;  Gaps    9;

Qy         53 LLALLSCCLTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAG-------LEEA 105
              :|  ::| : ::        | :| ||| |:    :    :|  : | |         |::
Db         29 VLGAVTCAVALL------IQQTELQSLRREV----SRLQRSGGPSQKQGERPWQSLWEQS 78

Qy        106 PAVTAGLKIFEPPAPGEGNSSQNSRNKRAVQGPEETVTQDCLQLI-------ADSETPTI 158
              | |    |               || :|||   :       | |:       |||:
Db         79 PDVLEAWK-----------DGAKSRRRAVLTQKHKKKHSVLHLVPVNITSKADSDV--- 124

Qy        159 QKGSYTFVPWLLSFKRGSALEEKENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVH 218
                 | | |    :||  || : : : | :|| : :| |||: | |: || :: |:
Db        125 -----TEVMWQPVLRRGRGLEAQGDIVRVWDTGIYLLYSQVLFHDVTFTMGQVVSRE--- 176

Qy        219 VFGDELSLVTLFRCIQNMPETLPN---NSCYSAGIAKLEEGDELQLAIPRENAQISLDGD 275
                :    ||||||::||   |:   |||||||:  | :|| : : ||| ||::||
Db        177 ---GQGRRETLFRCIRSMPSD-PDRAYNSCYSAGVFHLHQGDIITVKIPRANAKLSLSPH 232

Qy        276 VTFFGALKL 284
               || | :||
Db        233 GTFLGFVKL 241


RESULT 4
TN13_HUMAN
ID   TN13_HUMAN     STANDARD;      PRT;   250 AA.
AC   O75888; Q96HV6; Q9P1M8; Q9P1M9;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor ligand superfamily member 13 (A proliferation-
DE   inducing ligand) (APRIL) (TNF-and APOL-related leukocyte expressed
DE   ligand 2) (TALL-2) (TNF-related death ligand-1) (TRDL-1).
GN   TNFSF13 OR APRIL OR TALL2 OR ZTNF2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Uterus;
RX   MEDLINE=98416181; PubMed=9743536;
RA   Hahne M., Kataoka T., Schroeter M., Hofmann K., Irmler M.,
RA   Bodmer J.-L., Schneider P., Bornand T., Holler N., French L.E.,
RA   Sordat B., Rimoldi D., Tschopp J.;
RT   "APRIL, a new ligand of the tumor necrosis factor family, stimulates
RT   tumor cell growth.";
RL   J. Exp. Med. 188:1185-1190(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99260341; PubMed=10331498;
RA   Shu H.-B., Hu W.-H., Johnson H.;
RT   "TALL-1 is a novel member of the TNF family that is down-regulated by
RT   mitogens.";
RL   J. Leukoc. Biol. 65:680-683(1999).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Farrah T., Grant F., Haldeman B., Whitmore T., Gross J., O'Hara P.;
RT   "Homo sapiens tumor necrosis factor homolog.";
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORMS ALPHA; BETA AND GAMMA).
RX   MEDLINE=20168636; PubMed=10706119;
RA   Kelly K.A., Manos E.J., Jensen G.T., Nadauld L., Jones D.A.;
RT   "APRIL/TRDL-1, a tumor necrosis factor-like ligand, stimulates cell
RT   death.";
RL   Cancer Res. 60:1021-1027(2000).
RN   [5]
RP   SEQUENCE OF 1-247 FROM N.A.
RC   TISSUE=Ovary;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [6]
RP   FUNCTION.
RX   MEDLINE=21170294; PubMed=10973284;
RA   Yu G., Boone T., Delaney J., Hawkins N., Kelley M.J., Ramakrishnan M.,
RA   McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
RA   Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.;
RT   "APRIL and TALL-I and receptors BCMA and TACI: system for regulating
RT   humoral immunity.";
RL   Nat. Immunol. 1:252-256(2000).
RN   [7]
RP   PROCESSING BY FURIN, MUTAGENESIS OF ARG-101 AND ARG-104, AND
RP   SUBCELLULAR LOCATION.
RX   MEDLINE=21486098; PubMed=11571266;
RA   Lopez-Fraga M., Fernandez R., Albar J.P., Hahne M.;
RT   "Biologically active APRIL is secreted following intracellular
RT   processing in the Golgi apparatus by furin convertase.";
RL   EMBO Rep. 2:945-951(2001).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF13B/TACI and to
CC       TNFRSF17/BCMA. May be implicated in the regulation of tumor cell
CC       growth. May be involved in monocyte/macrophage-mediated
CC       immunological processes.
CC   -!- SUBUNIT: Homotrimer (Potential).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC       Name=Alpha;
CC         IsoId=O75888-1; Sequence=Displayed;
CC       Name=Beta;
CC         IsoId=O75888-2; Sequence=VSP_006450;
CC       Name=Gamma;
CC         IsoId=O75888-3; Sequence=VSP_006451;
CC   -!- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN TRANSFORMED CELL
CC       LINES, CANCERS OF COLON, THYROID, LYMPHOID TISSUES AND
CC       SPECIFICALLY EXPRESSED IN MONOCYTES AND MACROPHAGES.
CC   -!- INDUCTION: DOWN-REGULATED BY PHORBOL MYRISTATE ACETATE/IONOMYCIN
CC       TREATMENT.
CC   -!- PTM: The precursor is cleaved by furin.
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF046888; AAC61312.1; -.
DR   EMBL; AF136294; AAD29422.1; -.
DR   EMBL; AF184972; AAF01321.1; -.
DR   EMBL; AF114011; AAF59828.1; -.
DR   EMBL; AF114012; AAF59829.1; -.
DR   EMBL; AF114013; AAF59830.1; -.
DR   EMBL; BC008042; AAH08042.1; -.
DR   Genew; HGNC:11928; TNFSF13.
DR   MIM; 604472; -.
DR   GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR006052; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Immune response; Glycoprotein;
KW   Alternative splicing.
FT   PROPEP          1    104
FT   CHAIN         105    250       TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT                                   MEMBER 13.
FT   SITE          104    105       CLEAVAGE (BY FURIN).
FT   DISULFID      196    211       POTENTIAL.
FT   CARBOHYD      124    124       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC      113    129       KQHSVLHLVPINATSKD -> N (in isoform Beta).
FT                                   /FTId=VSP_006450.
FT   VARSPLIC      247    249       Missing (in isoform Gamma).
FT                                   /FTId=VSP_006451.
FT   MUTAGEN       101    104       RKRR->AKRA: ABOLISHES PROTEOLYTIC
FT                                   PROCESSING.
FT   CONFLICT       96     96       N -> S (IN REF. 5).
FT   CONFLICT      247    247       F -> L (IN REF. 5).
SQ   SEQUENCE   250 AA;  27433 MW;  AE1A6B9457F6E298 CRC64;

  Query Match             16.9%;  Score 244.5;  DB 1;  Length 250;
  Best Local Similarity   29.7%;  Pred. No. 1.2e-13;
  Matches   70;  Conservative   47;  Mismatches   90;  Indels   29;  Gaps    8;

Qy         54 LALLSCCLTVVSFYQVAALQGDLASLRAELQGHHAEKLPA--GAGAPKAGLEEAPAVTAG 111
              |  ::| : :::       | :| ||| |:        |:  | | |   | |    :
Db         39 LGAVACAMALLT------QQTELQSLRREVSRLQGTGGPSQNGEGYPWQSLPEQS--SDA 90

Qy        112 LKIFEPPAPGEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLS 171
              |: :|        : : || :|||   ::      | |:  : | :      | | | :
Db         91 LEAWE--------NGERSRKRRAVLTQKQKKQHSVLHLVPINAT-SKDDSDVTEVMWQPA 141

Qy        172 FKRGSALEEKENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFR 231
              :||  |: :   : ::: | : :| |||: | |: || :: |:       :    ||||
Db        142 LRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQVVSRE------GQGRQETLFR 195

Qy        232 CIQNMPETLPN---NSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKL 284
              ||::|| : |:   |||||||:  | :|| | : |||  |:::|    || | :||
Db        196 CIRSMP-SHPDRAYNSCYSAGVFHLHQGDILSVIIPRARAKLNLSPHGTFLGFVKL 250


RESULT 5
TNFA_CANFA
ID   TNFA_CANFA     STANDARD;      PRT;   233 AA.
AC   P51742; Q28339;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin).
GN   TNF OR TNFSF2 OR TNFA.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Fiers W.;
RT   "Tumour necrosis factor.";
RL   (In) Sim E. (eds.);
RL   The natural immune system humoral factors, pp.65-119, IRL Press,
RL   Oxford (1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Zucker K., Lu P., Fuller L., Asthana D., Esquenazi V., Miller J.;
RT   "Cloning and expression of the cDNA for canine tumor necrosis
```

```
RT   factor-alpha in E. coli.";
RL   Lymphokine Res. 13:191-196(1994).
RN   [3]
RP   SEQUENCE OF 74-205 FROM N.A.
RC   STRAIN=Beagle; TISSUE=Blood;
RA   Gilmore W.H., Carter S.D., Bennett M., Barnes A., Kelly D.F.;
RL   Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form ocurrs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC       CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC       AND MALNUTRITION.
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X94932; CAA64403.1; -.
DR   EMBL; S74068; AAB32391.1; -.
DR   EMBL; Z70046; CAA93908.1; -.
DR   HSSP; P01375; 4TSV.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Transmembrane; Signal-anchor; Phosphorylation.
FT   CHAIN         1    233       TUMOR NECROSIS FACTOR, MEMBRANE FORM.
FT   CHAIN        77    233       TUMOR NECROSIS FACTOR, SOLUBLE FORM.
FT   DOMAIN        1     35       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     36     56       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                 (POTENTIAL).
FT   DOMAIN       57    233       EXTRACELLULAR (POTENTIAL).
FT   SITE         76     77       CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT   MOD_RES       2      2       PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
FT   DISULFID    145    177       BY SIMILARITY.
FT   CONFLICT     59     60       QR -> PE (IN REF. 2).
FT   CONFLICT     66     66       G -> C (IN REF. 2).
FT   CONFLICT     74     74       A -> V (IN REF. 3).
FT   CONFLICT    111    111       A -> D (IN REF. 2).
FT   CONFLICT    116    116       G -> D (IN REF. 2).
FT   CONFLICT    134    135       IY -> DS (IN REF. 2).
SQ   SEQUENCE   233 AA;  25447 MW;  7B2588FBC8B25340 CRC64;

  Query Match             8.2%;  Score 118.5;  DB 1;  Length 233;
  Best Local Similarity   22.2%;  Pred. No. 0.006;
  Matches   54;  Conservative   37;  Mismatches   93;  Indels   59;  Gaps    9;

Qy         60 CLTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPA 119
              ||:: ||  ||       |   : |   |:||                  ||::  | |

Db         32 CLSLFSFLLVAGATTLFCLLHFGVIGPQREELP----------------NGLQLISPLA 74

Qy        120 PGEGNSSQNSRNK---RAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGS 176
                 :||:   :|      |  ||           |: :           : ||   :| :
Db         75 QTVKSSSRTPSDKPVAHVVANPE----------AEGQ----------LQWL--SRRAN 110

Qy        177 AL-----EEKENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFG----DELSLV 227
              ||     |  :|:::|   | : || |||:  :     |::    :  |      :::|:
Db        111 ALLANGVELTDNQLIVPSDGLYLIYSQVLFKGQGCPSTHVLLTHTISRFAVSYQTKVNLL 170

Qy        228 TLFR--CIQNMPETLPNNSCYS----AGIAKLEEGDELQLAIPRENAQISLDGDVTFFGA 281
              :  :  | :  ||       |      |: :||:|| |   |   |     :    :||
Db        171 SAIKSPCQRETPEGTEAKPWYEPIYLGGVFQLEKGDRLSAEINLPNYLDFAESGQVYFGI 230

Qy        282 LKL 284
              : |
Db        231 IAL 233


RESULT 6
TNFA_TURTR
ID   TNFA_TURTR     STANDARD;      PRT;   233 AA.
AC   Q9BEA1;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin).
GN   TNF OR TNFSF2 OR TNFA.
OS   Tursiops truncatus (Atlantic bottle-nosed dolphin).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC   Tursiops.
OX   NCBI_TaxID=9739;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21472839; PubMed=11587733;
RA   Shoji Y., Inoue Y., Sugisawa H., Itou T., Endo T., Sakai T.;
RT   "Molecular cloning and functional characterization of bottlenose
RT   dolphin (Tursiops truncatus) tumor necrosis factor alpha.";
RL   Vet. Immunol. Immunopathol. 82:183-192(2001).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation (By similarity).
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form ocurrs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB049358; BAB39855.1; -.
DR   HSSP; P01375; 4TSV.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
```

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DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Transmembrane; Signal-anchor; Phosphorylation.
FT   CHAIN         1    233       TUMOR NECROSIS FACTOR, MEMBRANE FORM.
FT   CHAIN        78    233       TUMOR NECROSIS FACTOR, SOLUBLE FORM.
FT   DOMAIN        1     35       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     36     56       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN       57    233       EXTRACELLULAR (POTENTIAL).
FT   SITE         77     78       CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT   MOD_RES       2      2       PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
FT   DISULFID    145    177       BY SIMILARITY.
FT   CARBOHYD     95     95       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   233 AA;  25404 MW;  71CC39C699CC49D9 CRC64;

  Query Match             8.0%;  Score 116.5;  DB 1;  Length 233;
  Best Local Similarity   22.7%;  Pred. No. 0.0089;
  Matches   56;  Conservative   38;  Mismatches   86;  Indels   67;  Gaps   10;

Qy         60 CLTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPA 119
              ||:: ||: ||        |   : |   |: |                   |  |  | |
Db         32 CLSLFSFFLVAGGTTLFCLLHFGVIGPQREEFP----------------TGYSIISPLA 74

Qy        120 PGEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKR---GS 176
                 :||: | ||          ||  |:                  || ::      :
Db         75 QTLRSSSKTSSNKPVAHVVANLSTQGQLR------------------WLNTYANTLLAN 115

Qy        177 ALEEKENKILVKETGYFFIYGQVLYTDKTYAMGHL-----IQRKKVHVFGDELSLVTLFR 231
                 ::: ::|:::|   | : || |||:  :     ||     | |  |  :  :::|::  :
Db        116 SVKLEDNQLVVPTDGLYLIYSQVLFRGQGCPSTHLFLTHTISRIAVS-YPSKVNLLSAIK 174

Qy        232 --CIQNMPETLP----NNSCYSAGIAKLEEGDELQLAIPRENAQISL--------DGDVT 277
                 | :  ||        |  |: :||:|| |       :|:|:|         | |
Db        175 SPCQRETPEGAEAKPWYEPIYQGGVFQLEKGDRL-------SAEINLPDYLDFAKSGQV- 226

Qy        278 FFGALKL 284
                :|| : |
Db        227 YFGIIAL 233


RESULT 7
TNFA_FELCA
ID   TNFA_FELCA     STANDARD;      PRT;   233 AA.
AC   P19101; Q8HYM0;
DT   01-NOV-1990 (Rel. 16, Created)
DT   15-SEP-2003 (Rel. 42, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin).
GN   TNF OR TNFSF2 OR TNFA.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=91016860; PubMed=2216740;
RA   McGraw R.A., Coffee B.W., Otto C.M., Drews R.T., Rawlings C.A.;
RT   "Gene sequence of feline tumor necrosis factor alpha.";
RL   Nucleic Acids Res. 18:5563-5563(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Bone marrow;
RA   Daniel S.L., Brenner C.A., Legendre A.M., Soloman A., Rouse B.T.;
RT   "Feline cytokines TNF alpha and IL-1 beta: PCR cloning and sequencing
RT   of cDNA.";
RL   Anim. Biotechnol. 3:117-121(1992).
RN   [3]
RP   SEQUENCE OF 95-185 FROM N.A.
RA   Susott E.E., Rollo W.A., Venta P.J., Ewart S.L.;
RT   "Characterization of 8 feline type I markers.";
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form ocurrs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC       CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC       AND MALNUTRITION.
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X54000; CAA37948.1; -.
DR   EMBL; M92061; AAA30818.1; -.
DR   EMBL; AF459810; AAO15590.1; -.
DR   PIR; S11688; S11688.
DR   HSSP; P01375; 4TSV.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Transmembrane; Signal-anchor; Phosphorylation.
FT   CHAIN         1    233       TUMOR NECROSIS FACTOR, MEMBRANE FORM.
FT   CHAIN        77    233       TUMOR NECROSIS FACTOR, SOLUBLE FORM.
FT   DOMAIN        1     35       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     36     56       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN       57    233       EXTRACELLULAR (POTENTIAL).
FT   SITE         76     77       CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT   MOD_RES       2      2       PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
FT   DISULFID    145    177       BY SIMILARITY.
FT   CONFLICT     28     28       G -> R (IN REF. 2).
FT   CONFLICT    104    104       W -> R (IN REF. 1).
FT   CONFLICT    141    141       T -> K (IN REF. 3).
FT   CONFLICT    151    151       L -> H (IN REF. 2).
FT   CONFLICT    155    155       T -> A (IN REF. 1).
FT   CONFLICT    210    210       T -> A (IN REF. 2).
SQ   SEQUENCE   233 AA;  25382 MW;  03E51823A7863510 CRC64;

  Query Match             7.7%;  Score 111.5;  DB 1;  Length 233;
  Best Local Similarity   23.5%;  Pred. No. 0.024;
  Matches   58;  Conservative   35;  Mismatches   87;  Indels   67;  Gaps   12;

Qy         60 CLTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPA 119
              ||:: ||  ||        |   : |   |:||                  ||::  |
Db         32 CLSLFSFLLVAGATTLFCLLHFGVIGPQREELP----------------HGLQLINPLP 74

Qy        120 PGEGNSSQNSRNK---RAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGS 176
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              :||:   :|     |  ||           |: :           : ||   :| :
Db         75 QTLRSSSRTPSDKPVAHVVANPE----------AEGQ----------LQWL--SRRAN 110

Qy        177 AL-----EEKENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFG----DELSLV 227
              ||     | :|:: |   | : || |||:| :     |::    : |      :::|:
Db        111 ALLANGVELTDNQLKVPSDGLYLIYSQVLFTGQGCPSTHVLLTHTISRFAVSYQTKVNLL 170

Qy        228 TLFR--CIQNMPETLPNNSCYS----AGIAKLEEGDELQLAIPRENAQISLD----GDVT 277
              .  :  :  | :  ||       |      |: :||:|| |   |   |    ||    | |
Db        171 SAIKSPCQRETPEGAEAKPWYEPIYLGGVFQLEKGDRLSTEI---NLPAYLDFAESGQV- 226

Qy        278 FFGALKL 284
              :|| : |
Db        227 YFGIIAL 233
```

RESULT 8
TNFA_DELLE
ID TNFA_DELLE STANDARD; PRT; 233 AA.
AC Q8WNR1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE ligand superfamily member 2) (TNF-a) (Cachectin).
GN TNF OR TNFSF2 OR TNFA.
OS Delphinapterus leucas (Beluga whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
OC Monodontidae; Delphinapterus.
OX NCBI_TaxID=9749;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21618234; PubMed=11768130;
RA Denis F., Archambault D.;
RT "Molecular cloning and characterization of beluga whale
RT (Delphinapterus leucas) interleukin-1beta and tumor necrosis
RT factor-alpha.";
RL Can. J. Vet. Res. 65:233-240(2001).
CC -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia, Under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation (By similarity).
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- PTM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form ocurrs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC ---
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CC or send an email to license@isb-sib.ch).
CC ---
DR EMBL; AF320323; AAL56946.1; -.
DR InterPro; IPR006053; TNF_abc.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Transmembrane; Signal-anchor; Phosphorylation.
FT CHAIN 1 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
FT CHAIN 78 233 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 57 233 EXTRACELLULAR (POTENTIAL).
FT SITE 77 78 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT MOD_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
FT DISULFID 145 177 BY SIMILARITY.
FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 233 AA; 25420 MW; 2DF37DCB2BC9E961 CRC64;

Query Match 7.6%; Score 110.5; DB 1; Length 233;
Best Local Similarity 22.0%; Pred. No. 0.029;
Matches 54; Conservative 40; Mismatches 87; Indels 65; Gaps 10;

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Qy         60 CLTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPA 119
              ||:: ||: ||       |   : |   |: |                  | | | |
Db         32 CLSLFSFFLVAGGTTLFCLLHFGVIGPQREEFP----------------TGYSIISPLA 74

Qy        120 PGEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKR---GS 176
                 :||: | ||         |     | |  :          : || ::      :
Db         75 QTLRSSSKTSSNK--------PVAHVVANLSAQGQ----------LRWLNTYANTLLAN 115

Qy        177 ALEEKENKILVKETGYFFIYGQVLYTDKTYAMGHL-----IQRKKVHVFGDELSLVTLFR 231
              ::: ::|:::|   | : || |||:  :     ||     | | | :  :::|::  :
Db        116 SVKLEDNQLVVPTDGLYLIYSQVLFRGQGCPSTHLFLTHTISRIAVS-YQTKVNLLSAIK 174

Qy        232 --CIQNMPETLP----NNSCYSAGIAKLEEGDELQLAIPRENAQISL-------DGDVTF 278
                | :  ||         |  |: :||:|| |       :|:|:|       :    :
Db        175 SPCQRETPEGAEAKPWYEPIYQGGVFQLEKGDRL-------SAEINLPDYLDFAESGQVY 227

Qy        279 FGALKL 284
              || : |
Db        228 FGIIAL 233
```

RESULT 9
TNFA_RAT
ID TNFA_RAT STANDARD; PRT; 235 AA.
AC P16599; Q9JI26; Q9JI27;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE ligand superfamily member 2) (TNF-a) (Cachectin).
GN TNF OR TNFSF2 OR TNFA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Shirai T., Shimizu N., Horiguchi S., Ito H.;
RT "Cloning and expression in Escherichia coli of the gene for rat tumor
RT necrosis factor.";
RL Agric. Biol. Chem. 53:1733-1736(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92329007; PubMed=1627266;
RA Estler H.C., Grewe M., Gaussling R., Pavlovic M., Decker K.;
RT "Rat tumor necrosis factor-alpha. Transcription in rat Kupffer cells
RT and in vitro posttranslational processing based on a PCR-derived
RT cDNA.";
RL Biol. Chem. Hoppe-Seyler 373:271-281(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Testis;
RX MEDLINE=94040766; PubMed=8224868;
RA Kwon J., Chung I.Y., Benveniste E.N.;

```
RT   "Cloning and sequence analysis of the rat tumor necrosis
RT   factor-encoding genes.";
RL   Gene 132:227-236(1993).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ACI/SegHsd, BB(DR)/Wor, BN/SsNHsd, DA/Bkl, F344/NHsd, and
RC   LEW/NHsd;
RX   MEDLINE=21369712; PubMed=11477479;
RA   Furuya T., Joe B., Salstrom J.L., Hashiramoto A., Dobbins D.E.,
RA   Wilder R.L., Remmers E.F.;
RT   "Polymorphisms of the tumor necrosis factor alpha locus among
RT   autoimmune disease susceptible and resistant inbred rat strains.";
RL   Genes Immun. 2:229-232(2001).
RN   [5]
RP   SEQUENCE FROM N.A.
RA   Decker K.F.;
RL   Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A., AND VARIANTS PRO-122 AND GLU-190.
RC   STRAIN=Dark Agouti;
RA   Seidel M.F., Junier M.-P., Vetter H.;
RT   "TNF-alpha polymorphism in rats with collagen-induced arthritis.";
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   SEQUENCE OF 1-231 FROM N.A.
RC   TISSUE=Tail;
RA   Kirisits M.J., Vardimon D., Kunz H.W., Gill T.J. III;
RL   Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form ocurrs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC       CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC       AND MALNUTRITION.
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D00475; BAA00367.1; -.
DR   EMBL; X66539; CAA47146.1; -.
DR   EMBL; L00981; AAA16275.1; -.
DR   EMBL; AF329982; AAK53568.1; -.
DR   EMBL; AF329983; AAK53569.1; -.
DR   EMBL; AF329984; AAK53570.1; -.
DR   EMBL; AF329985; AAK53571.1; -.
DR   EMBL; AF329986; AAK53572.1; -.
DR   EMBL; AF329987; AAK53573.1; -.
DR   EMBL; AJ002278; CAA05290.1; -.
DR   EMBL; AF269159; AAF82567.1; -.
DR   EMBL; AF269160; AAF82568.1; -.
DR   EMBL; L19123; AAA42255.1; -.
DR   PIR; JU0029; JU0029.
DR   HSSP; P06804; 2TNF.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Transmembrane; Signal-anchor; Phosphorylation.
FT   CHAIN         1    235       TUMOR NECROSIS FACTOR, MEMBRANE FORM.
FT   CHAIN        80    235       TUMOR NECROSIS FACTOR, SOLUBLE FORM.
FT   DOMAIN        1     35       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     36     56       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                 (POTENTIAL).
FT   DOMAIN       57    235       EXTRACELLULAR (POTENTIAL).
FT   SITE         79     80       CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT   MOD_RES       2      2       PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
FT   DISULFID    148    179       BY SIMILARITY.
FT   CARBOHYD     86     86       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT     122    122       L -> P.
FT   VARIANT     190    190       K -> E.
FT   CONFLICT     39     39       L -> P (IN REF. 2 AND 5).
FT   CONFLICT    163    163       I -> T (IN REF. 2 AND 5).
FT   CONFLICT    202    202       F -> S (IN REF. 2 AND 5).
SQ   SEQUENCE   235 AA;  25806 MW;  B808EC6D049C2F3B CRC64;

  Query Match             7.6%;  Score 110.5;  DB 1;  Length 235;
  Best Local Similarity   22.2%;  Pred. No. 0.029;
  Matches   54;  Conservative   45;  Mismatches   87;  Indels   57;  Gaps   11;

Qy         60 CLTVVSFYQVAALQGDLASLRAELQG-HHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPP 118
              ||:: ||  ||         |   : | :  || | |       |  : | |  |:
Db         32 CLSLFSFLLVAGATTLFCLLNFGVIGPNKEEKFPNG-----LPLISSMAQTLTLR----- 81

Qy        119 APGEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSAL 178
                 :||||| :|           :: |: ::      :  |                :
Db         82 -----SSSQNSSDKPVAHVVANHQAEEQLEWLSQRANALLANG---------------M 120

Qy        179 EEKENKILVKETGYFFIYGQVLYTDK----TYAMGHLIQRKKVHVFGDELSLVTLFR--C 232
               : |:|:::|   | : || |||:  :     : | : |  :  : :::||::  :  |
Db        121 DLKDNQLVVPADGLYLIYSQVLFKGQGCPDYVLLTHTVSRFAIS-YQEKVSLLSAIKSPC 179

Qy        233 IQNMPETLP----NNSCYSAGIAKLEEGDELQLAIPRENAQISLDG--DVT-----FFGA 281
               :: ||          |  |: :||:|| |       :|:::|    |:|     :||
Db        180 PKDTPEGAELKPWYEPMYLGGVFQLEKGDLL------SAEVNLPKYLDITESGQVYFGV 232

Qy        282 LKL 284
               : |
Db        233 IAL 235


RESULT 10
TNFA_MOUSE
ID   TNFA_MOUSE     STANDARD;      PRT;   235 AA.
AC   P06804; O35853; Q62326; Q91VF3;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-MAR-1989 (Rel. 10, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin).
GN   TNF OR TNFSF2 OR TNFA.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88224564; PubMed=2836146;
RA   Shirai T., Shimizu N., Shiojiri S., Horiguchi S., Ito H.;
RT   "Cloning and expression in Escherichia coli of the gene for mouse
RT   tumor necrosis factor.";
RL   DNA 7:193-201(1988).
RN   [2]
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RP   SEQUENCE FROM N.A.
RX   MEDLINE=85298296; PubMed=3898078;
RA   Pennica D., Hayflick J.S., Bringman T.S., Palladino M.A.,
RA   Goeddel D.V.;
RT   "Cloning and expression in Escherichia coli of the cDNA for murine
RT   tumor necrosis factor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 82:6060-6064(1985).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86149365; PubMed=2419912;
RA   Caput D., Beutler B., Hartog K., Thayer R., Brown-Shimer S.,
RA   Cerami A.;
RT   "Identification of a common nucleotide sequence in the
RT   3'-untranslated region of mRNA molecules specifying inflammatory
RT   mediators.";
RL   Proc. Natl. Acad. Sci. U.S.A. 83:1670-1674(1986).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85242112; PubMed=2989794;
RA   Fransen L., Mueller R., Marmenout A., Tavernier J., van der Heyden J.,
RA   Kawashima E., Chollet A., Tizard R., van Heuverswyn H., van Vliet A.,
RA   Ruysschaert M.-R., Fiers W.;
RT   "Molecular cloning of mouse tumour necrosis factor cDNA and its
RT   eukaryotic expression.";
RL   Nucleic Acids Res. 13:4417-4429(1985).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87298639; PubMed=3040015;
RA   Shakhov A.N., Nedospasov S.A.;
RT   "Molecular cloning of genes coding for tumor necrosis factor.
RT   Complete nucleotide sequence of the genome copy of TNF-alpha in
RT   mice.";
RL   Bioorg. Khim. 13:701-705(1987).
RN   [6]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88067722; PubMed=3684584;
RA   Semon D., Kawashima E., Jongeneel C.V., Shakhov A.N., Nedospasov S.A.;
RT   "Nucleotide sequence of the murine TNF locus, including the TNF-alpha
RT   (tumor necrosis factor) and TNF-beta (lymphotoxin) genes.";
RL   Nucleic Acids Res. 15:9083-9084(1987).
RN   [7]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CTS, and NOD;
RX   MEDLINE=96013654; PubMed=7560085;
RA   Ikegami H., Makino S., Yamato E., Kawaguchi Y., Ueda H., Sakamoto T.,
RA   Takekawa K., Ogihara T.;
RT   "Identification of a new susceptibility locus for insulin-dependent
RT   diabetes mellitus by ancestral haplotype congenic mapping.";
RL   J. Clin. Invest. 96:1936-1942(1995).
RN   [8]
RP   SEQUENCE FROM N.A., AND VARIANTS THR-7 AND ALA-77.
RC   STRAIN=A/J, BALB/c, and C57BL/6;
RX   MEDLINE=97246744; PubMed=9089109;
RA   Iraqi F., Teale A.;
RT   "Cloning and sequencing of the Tnfa genes of three inbred mouse
RT   strains.";
RL   Immunogenetics 45:459-461(1997).
RN   [9]
RP   SEQUENCE FROM N.A.
RA   Rowen L., Qin S., Madan A., Abbasi N., James R., Dickhoff R.,
RA   Shaffer T., Ratcliffe A., Loretz C., Lasky S., Hood L.;
RT   "Sequence of the mouse major histocompatibility class III region.";
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
RN   [10]
RP   SEQUENCE OF 1-96 FROM N.A.
RC   STRAIN=BLG2/Msf, BFM/2Msf, C57BL/10SnJ, CAST/Ei, HMI/Msf, MSM/Msf,
RC   NJL/Msf, pgn2, and SWN/Msf;
RA   Liu Y., Kitano T., Koide T., Shiroishi T., Moriwaki K., Saitou N.;
RT   "Conspicuous differences among gene genealogies of 21 nuclear genes of
RT   five Mus musculus subspecies.";
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
RN   [11]
RP   SEQUENCE OF 70-87.
RX   MEDLINE=89380231; PubMed=2777790;
RA   Cseh K., Beutler B.;
RT   "Alternative cleavage of the cachectin/tumor necrosis factor
RT   propeptide results in a larger, inactive form of secreted protein.";
RL   J. Biol. Chem. 264:16256-16260(1989).
RN   [12]
RP   SEQUENCE OF 80-99.
RX   MEDLINE=91097531; PubMed=2268312;
RA   Sherry B., Juc D.-M., Zentella A., Cerami A.;
RT   "Characterization of high molecular weight glycosylated forms of
RT   murine tumor necrosis factor.";
RL   Biochem. Biophys. Res. Commun. 173:1072-1078(1990).
RN   [13]
RP   IDENTIFICATION OF MEMBRANE-BOUND FORM.
RX   MEDLINE=88165056; PubMed=3349526;
RA   Kriegler M., Perez X., Defay K., Albert I., Lu S.D.;
RT   "A novel form of TNF/cachectin is a cell surface cytotoxic
RT   transmembrane protein: ramifications for the complex physiology of
RT   TNF.";
RL   Cell 53:45-53(1988).
RN   [14]
RP   X-RAY CRYSTALLOGRAPHY (1.4 ANGSTROMS) OF 80-235.
RX   MEDLINE=99190964; PubMed=10089307;
RA   Baeyens K.J., De Bondt H.L., Raeymaekers A., Fiers W., De Ranter C.J.;
RT   "The structure of mouse tumour-necrosis factor at 1.4 A resolution:
RT   towards modulation of its selectivity and trimerization.";
RL   Acta Crystallogr. D 55:772-778(1999).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation.
CC   -!- SUBUNIT: Homotrimer.
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form.
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing.
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form ocurrs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC       CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC       AND MALNUTRITION.
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M20155; AAA40462.1; ALT_SEQ.
DR   EMBL; M11731; AAA40458.1; -.
DR   EMBL; M13049; AAA40457.1; -.
DR   EMBL; X02611; CAA26457.1; -.
DR   EMBL; M38296; AAA40459.1; -.
DR   EMBL; Y00467; CAA68530.1; -.
DR   EMBL; U06950; AAA18594.1; -.
DR   EMBL; D84196; BAA19512.1; -.
DR   EMBL; D84194; BAA19512.1; JOINED.
DR   EMBL; D84195; BAA19512.1; JOINED.
DR   EMBL; D84199; BAA19513.1; -.
DR   EMBL; D84197; BAA19513.1; JOINED.
DR   EMBL; D84198; BAA19513.1; JOINED.
DR   EMBL; U68414; AAB65593.1; -.
DR   EMBL; AF109719; AAC82484.1; -.
DR   EMBL; AB039224; BAB68748.1; ALT_SEQ.
DR   EMBL; AB039225; BAB68749.1; ALT_SEQ.
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DR   EMBL; AB039226; BAB68750.1; ALT_SEQ.
DR   EMBL; AB039227; BAB68751.1; ALT_SEQ.
DR   EMBL; AB039228; BAB68752.1; ALT_SEQ.
DR   EMBL; AB039229; BAB68753.1; ALT_SEQ.
DR   EMBL; AB039230; BAB68754.1; ALT_SEQ.
DR   EMBL; AB039231; BAB68755.1; ALT_SEQ.
DR   EMBL; AB039232; BAB68756.1; ALT_SEQ.
DR   PIR; A22908; QWMSN.
DR   PDB; 2TNF; 12-OCT-99.
DR   MGD; MGI:104798; Tnf.
DR   GO; GO:0007275; P:development; IMP.
DR   GO; GO:0006959; P:humoral immune response; IMP.
DR   GO; GO:0009887; P:organogenesis; IMP.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Transmembrane; Signal-anchor; Phosphorylation; Glycoprotein;
KW   Polymorphism; 3D-structure.
FT   CHAIN         1    235       TUMOR NECROSIS FACTOR, MEMBRANE FORM.
FT   CHAIN        80    235       TUMOR NECROSIS FACTOR, SOLUBLE FORM.
FT   DOMAIN        1     35       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     36     56       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN       57    235       EXTRACELLULAR (POTENTIAL).
FT   SITE         79     80       CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT   MOD_RES       2      2       PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
FT   DISULFID    148    179
FT   CARBOHYD     86     86       N-LINKED (GLCNAC. . .).

  Query Match             7.5%;  Score 109.5;  DB 1;  Length 235;
  Best Local Similarity   21.0%;  Pred. No. 0.036;
  Matches   51;  Conservative   48;  Mismatches   87;  Indels   57;  Gaps   11;

Qy         60 CLTVVSFYQVAALQGDLASLRAELQG-HHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPP 118
              ||:: ||  ||        |   : |    || | |       |  : | |  |:
Db         32 CLSLFSFLLVAGATTLFCLLNFGVIGPQRDEKFPNG-----LPLISSMAQTLTLR----- 81

Qy        119 APGEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSAL 178
                  :||||| :|          :: |: ::      :  |               :
Db         82 -----SSSQNSSDKPVAHVVANHQVEEQLEWLSQRANALLANG---------------M 120

Qy        179 EEKENKILVKETGYFFIYGQVLYTDK----TYAMGHLIQRKKVHVFGDELSLVTLFR--C 232
             : |:|:::|   | : :| |||:  :       : | : |  :  : ::::|::  :  |
Db        121 DLKDNQLVVPADGLYLVYSQVLFKGQGCPDYVLLTHTVSRFAIS-YQEKVNLLSAVKSPC 179

Qy        233 IQNMPETLP----NNSCYSAGIAKLEEGDEL--QLAIPR-----ENAQISLDGDVTFFGA 281
              :: ||          |  |: :||:||:|  :: :|:     |: |:       :||
Db        180 PKDTPEGAELKPWYEPIYLGGVFQLEKGDQLSAEVNLPKYLDFAESGQV-------YFGV 232

Qy        282 LKL 284
             : |
Db        233 IAL 235


RESULT 11
TNFA_BOVIN
ID   TNFA_BOVIN     STANDARD;      PRT;   233 AA.
AC   Q06599; O18779; Q27978;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin).
GN   TNF OR TNFSF2 OR TNFA.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94083525; PubMed=8260599;
RA   Cludts I., Cleuter Y., Kettmann R., Burny A., Droogmans L.;
RT   "Cloning and characterization of the tandemly arranged bovine
RT   lymphotoxin and tumour necrosis factor-alpha genes.";
RL   Cytokine 5:336-341(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Boran, and N'Dama;
RA   Iraqi F.;
RT   "Bovine TNF-alpha gene.";
RL   Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Ahn J.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE OF 50-233 FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=96006582; PubMed=7590981;
RA   Mertens B.E.L.C., Muriuki M., Gaidulis L.;
RT   "Cloning of two members of the TNF-superfamily in cattle: CD40 ligand
RT   and tumor necrosis factor alpha.";
RL   Immunogenetics 42:430-431(1995).
RN   [5]
RP   SEQUENCE OF 89-193 FROM N.A.
RC   STRAIN=Holstein;
RX   PubMed=9303477;
RA   Dietz A.B., Neibergs H.L., Womack J.E., Kehrli M.E. Jr.;
RT   "Rapid communication: single strand conformational polymorphism (SSCP)
RT   of bovine tumor necrosis factor alpha.";
RL   J. Anim. Sci. 75:2567-2567(1997).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form ocurrs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC       CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC       AND MALNUTRITION.
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z14137; CAA78511.1; -.
DR   EMBL; AF011926; AAB84086.1; -.
DR   EMBL; AF348421; AAN76506.1; -.
DR   EMBL; AF011927; AAB84087.1; -.
DR   EMBL; Z48808; CAA88743.1; -.
DR   EMBL; U11040; AAA19573.1; ALT_SEQ.
DR   PIR; I46047; S24642.
DR   HSSP; P01375; 4TSV.
DR   InterPro; IPR006053; TNF_abc.
```

```
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Transmembrane; Signal-anchor; Phosphorylation; Polymorphism.
FT   CHAIN         1    233       TUMOR NECROSIS FACTOR, MEMBRANE FORM.
FT   CHAIN        77    233       TUMOR NECROSIS FACTOR, SOLUBLE FORM.
FT   DOMAIN        1     35       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     36     56       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN       57    233       EXTRACELLULAR (POTENTIAL).
FT   SITE         76     77       CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT   MOD_RES       2      2       PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
FT   DISULFID    145    177       BY SIMILARITY.
FT   VARIANT      48     48       F -> C (IN STRAIN N'DAMA).
FT   CONFLICT     62     62       E -> EQ (IN REF. 3 AND 4).
FT   CONFLICT    113    113       M -> V (IN REF. 3).
FT   CONFLICT    166    166       K -> R (IN REF. 3).
SQ   SEQUENCE   233 AA;  25439 MW;  8AF55C002A9763B0 CRC64;

  Query Match             7.4%;  Score 108;  DB 1;  Length 233;
  Best Local Similarity   22.8%;  Pred. No. 0.047;
  Matches   56;  Conservative   42;  Mismatches   88;  Indels   60;  Gaps   12;

Qy         58 SC-CLTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFE 116
              || ||:: ||  ||        |   : |   |: | |           |:: :
Db         29 SCLCLSLFSFLLVAGATTLFCLLHFGVIGPQREESPGG----------PSINS------ 71

Qy        117 PPAPGEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGS 176
              |      :||| | ||              ::||  :|  :   ::   |::   |
Db         72 PLVQTLRSSSQASSNKPVA-----------HVVADINSPGQLRWWDSYANALMA--NGV 117

Qy        177 ALEEKENKILVKETGYFFIYGQVLYTDK-----TYAMGHLIQRKKVHVFGDELSLVTLFR 231
              ||  :|:::|   | : || |||:  :        : | | |  |  :  :::::  :
Db        118 KLE--DNQLVVPADGLYLIYSQVLFRGQGCPSTPLFLTHTISRIAVS-YQTKVNILSAIK 174

Qy        232 --CIQNMPETLP----NNSCYSAGIAKLEEGDELQLAIPRENAQISL-------DGDVTF 278
                | :  ||           |  |: :||:|| |       :|:|:|       :   :
Db        175 SPCHRETPEWAEAKPWYEPIYQGGVFQLEKGDRL-------SAEINLPDYLDYAESGQVY 227

Qy        279 FGALKL 284
              || : |
Db        228 FGIIAL 233


RESULT 12
TNFA_PERLE
ID   TNFA_PERLE     STANDARD;      PRT;   235 AA.
AC   P36939;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin).
GN   TNF OR TNFSF2 OR TNFA.
OS   Peromyscus leucopus (White-footed mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC   Peromyscus.
OX   NCBI_TaxID=10041;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92218012; PubMed=1348497;
RA   Crew M.D., Filipowsky M.E.;
RT   "Sequence of the tumor necrosis factor/cachectin (TNF) gene from
RT   Peromyscus leucopus (family Cricetidae).";
RL   Immunogenetics 35:351-353(1992).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form ocurrs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC       CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC       AND MALNUTRITION.
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M59233; AAA40596.1; -.
DR   PIR; I54490; I54490.
DR   HSSP; P06804; 2TNF.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Transmembrane; Signal-anchor; Phosphorylation.
FT   CHAIN         1    235       TUMOR NECROSIS FACTOR, MEMBRANE FORM.
FT   CHAIN        80    235       TUMOR NECROSIS FACTOR, SOLUBLE FORM.
FT   DOMAIN        1     35       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     36     56       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN       57    235       EXTRACELLULAR (POTENTIAL).
FT   SITE         79     80       CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT   MOD_RES       2      2       PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
FT   DISULFID    148    179       BY SIMILARITY.
FT   CARBOHYD     86     86       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   235 AA;  25822 MW;  235A5CFC9F9AC624 CRC64;

  Query Match             7.4%;  Score 107.5;  DB 1;  Length 235;
  Best Local Similarity   22.0%;  Pred. No. 0.053;
  Matches   54;  Conservative   46;  Mismatches   84;  Indels   61;  Gaps   14;

Qy         60 CLTVVSFYQVAALQGDLASLRAELQG-HHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPP 118
              ||:: ||  ||        |   : |    || |     |  |   : | |  |:
Db         32 CLSLFSFLLVAGATTLFCLLNFGVIGPQREEKFP--NNLPIIG---SMAQTLTLR----- 81

Qy        119 APGEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSAL 178
                  :||||| :|         |         | :   : :|:   :         : :
Db         82 -----SSSQNSSDK--------PVAHVVANHQVDEQLEWLSRGANALL--------ANGM 120

Qy        179 EEKENKILVKETGYFFIYGQVLYTDK---TYA-MGHLIQRKKVHVFGDELSLVTLFRCIQ 234
              : |:|::::   | : :| |||:  :   :|  : | : |  |  : |:::|::  :
Db        121 DLKDNQLVIPADGLYLVYSQVLFKGQGCSSYVLLTHTVSRFAVS-YEDKVNLLSAIK--S 177

Qy        235 NMPETLPNNS--------CYSAGIAKLEEGDEL--QLAIPR-----ENAQISLDGDVTFF 279
                |:  |  |         |  |: :||:|| |  :: :|:     |: |:       :|
Db        178 PCPKETPEGSELKPWYEPIYLGGVFQLEKGDRLSAEVNLPKYLDFAESGQV-------YF 230

Qy        280 GALKL 284
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                | : |
Db        231 GVIAL 235


RESULT 13
TNFA_PIG
ID   TNFA_PIG       STANDARD;      PRT;   232 AA.
AC   P23563;
DT   01-NOV-1991 (Rel. 20, Created)
DT   01-NOV-1991 (Rel. 20, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin).
GN   TNF OR TNFSF2 OR TNFA.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91016861; PubMed=2216741;
RA   Drews R.T., Coffee B.W., Prestwood A.K., McGraw R.A.;
RT   "Gene sequence of porcine tumor necrosis factor alpha.";
RL   Nucleic Acids Res. 18:5564-5564(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=91340150; PubMed=1874444;
RA   Kuhnert P., Wuethrich C., Peterhans E., Pauli U.;
RT   "The porcine tumor necrosis factor-encoding genes: sequence and
RT   comparative analysis.";
RL   Gene 102:171-178(1991).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Macrophage;
RA   Choi C.S., Molitor T.W., Lin G.F., Murtaugh M.P.;
RT   "Complete nucleotide sequence of a cDNA encoding porcine tumor
RT   necrosis factor-alpha.";
RL   Anim. Biotechnol. 2:97-105(1991).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Large white; TISSUE=Fibroblast;
RX   MEDLINE=21108615; PubMed=11169259;
RA   Chardon P., Rogel-Gaillard C., Cattolico L., Duprat S., Vaiman M.,
RA   Renard C.;
RT   "Sequence of the swine major histocompatibility complex region
RT   containing all non-classical class I genes.";
RL   Tissue Antigens 57:55-65(2001).
RN   [5]
RP   SEQUENCE OF 44-232 FROM N.A.
RX   MEDLINE=90034181; PubMed=2478420;
RA   Pauli U., Beutler B., Peterhans E.;
RT   "Porcine tumor necrosis factor alpha: cloning with the polymerase
RT   chain reaction and determination of the nucleotide sequence.";
RL   Gene 81:185-191(1989).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form ocurrs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC       CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC       AND MALNUTRITION.
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X54001; CAA37949.1; -.
DR   EMBL; X54859; CAA38639.1; -.
DR   EMBL; X57321; CAA40591.1; -.
DR   EMBL; AJ251914; CAB63852.1; -.
DR   EMBL; M29079; AAA31128.1; -.
DR   PIR; S12606; S12606.
DR   HSSP; P01375; 4TSV.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Transmembrane; Signal-anchor; Phosphorylation.
FT   CHAIN         1    232       TUMOR NECROSIS FACTOR, MEMBRANE FORM.
FT   CHAIN        77    232       TUMOR NECROSIS FACTOR, SOLUBLE FORM.
FT   DOMAIN        1     35       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     36     56       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN       57    232       EXTRACELLULAR (POTENTIAL).
FT   SITE         76     77       CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT   MOD_RES       2      2       PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
FT   DISULFID    144    176       BY SIMILARITY.
SQ   SEQUENCE   232 AA;  25254 MW;  65B28F702D99C8BE CRC64;

  Query Match             7.4%;  Score 107;  DB 1;  Length 232;
  Best Local Similarity   22.0%;  Pred. No. 0.057;
  Matches   54;  Conservative   40;  Mismatches   86;  Indels   66;  Gaps   11;

Qy         60 CLTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPA 119
              ||:: ||  ||        |  |: |   |: |||                | |  | |
Db         32 CLSLFSFLLVAGATTLFCLLHFEVIGPQKEEFPAGP---------------LSI-NPLA 74

Qy        120 PGEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKR---GS 176
               |  :||| |          :: |      : |: :           : |   :      :
Db         75 QGLRSSSQTS---------DKPVAHVVANVKAEGQ----------LQWQSGYANALLAN 114

Qy        177 ALEEKENKILVKETGYFFIYGQVLYTDK-----TYAMGHLIQRKKVHVFGDELSLVTLFR 231
              :: |:|:::|   | : || |||:  :        : | | |  |  :  :::|::  :
Db        115 GVKLKDNQLVVPTDGLYLIYSQVLFRGQGCPSTNVFLTHTISRIAVS-YQTKVNLLSAIK 173

Qy        232 --CIQNMPETLPNNSCYS----AGIAKLEEGDELQLAIPRENAQISL-------DGDVTF 278
                | :  ||        |      |: :||: | |       :|:|:|       :    :
Db        174 SPCQRETPEGAEAKPWYEPIYLGGVFQLEKDDRL-------SAEINLPDYLDFAESGQVY 226

Qy        279 FGALKL 284
               || : |
Db        227 FGIIAL 232


RESULT 14
TNFA_CAPHI
ID   TNFA_CAPHI     STANDARD;      PRT;   234 AA.
AC   P13296; Q28320; Q9MYZ2;
DT   01-JAN-1990 (Rel. 13, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin).
```

```
GN   TNF OR TNFSF2 OR TNFA.
OS   Capra hircus (Goat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Capra.
OX   NCBI_TaxID=9925;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Splenocyte;
RA   Takakura H., Mori Y., Tatsumi M.;
RT   "Molecular cloning of caprine TNF-alpha cDNA and its expression in
RT   E.coli and insect cells.";
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 41-234 FROM N.A.
RA   Goldstein I.M., Henner D., Talhouk A.;
RL   Submitted (MAR-1989) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE OF 44-234 FROM N.A.
RC   TISSUE=Ovarian follicle;
RA   Wang B., Zhang Y.;
RT   "Goat ovarian TNF alpha cDNA sequence.";
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE OF 75-234 FROM N.A.
RC   TISSUE=Blood;
RA   Rimstad E.;
RL   Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form ocurrs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC       CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC       AND MALNUTRITION.
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   -!- CAUTION: Ref.2 sequence differs from that shown due to a
CC       frameshift in position 60.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D86587; BAA13130.1; -.
DR   EMBL; X14828; CAA32937.1; ALT_FRAME.
DR   EMBL; AF276985; AAF87741.1; -.
DR   EMBL; X77317; CAA54523.1; -.
DR   HSSP; P01375; 4TSV.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Transmembrane; Signal-anchor; Phosphorylation.
FT   CHAIN         1    234       TUMOR NECROSIS FACTOR, MEMBRANE FORM.
FT   CHAIN        79    234       TUMOR NECROSIS FACTOR, SOLUBLE FORM.
FT   DOMAIN        1     35       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     36     56       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN       57    233       EXTRACELLULAR (POTENTIAL).
FT   MOD_RES       2      2       PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
FT   SITE         78     79       CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT   DISULFID    146    178       BY SIMILARITY.
FT   CARBOHYD     96     96       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     79     79       R -> S (IN REF. 4).
FT   CONFLICT    119    119       E -> A (IN REF. 4).
FT   CONFLICT    129    129       T -> N (IN REF. 4).
FT   CONFLICT    155    155       H -> Q (IN REF. 4).
FT   CONFLICT    164    164       Y -> D (IN REF. 4).
FT   CONFLICT    184    184       E -> EG (IN REF. 4).
FT   CONFLICT    185    185       MISSING (IN REF. 2).
FT   CONFLICT    215    215       Q -> L (IN REF. 3 AND 4).
SQ   SEQUENCE   234 AA;  25519 MW;  9768E33BBBABB041 CRC64;

  Query Match          7.3%;  Score 106.5;  DB 1;  Length 234;
  Best Local Similarity   22.2%;  Pred. No. 0.064;
  Matches   53;  Conservative   37;  Mismatches  104;  Indels   45;  Gaps    9;

Qy         58 SC-CLTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFE 116
              || ||:: ||  ||          |   :|  |              |::|   ||
Db         29 SCWCLSLFSFLLVAGATTLFCLLHFGVIGPQRE------------EQSP---AGPSFNR 72

Qy        117 PPAPGEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGS 176
              |      :||| | ||               ::|:   |    |   :    :  : :
Db         73 PLVQTLRSSSQASSNKPVA-----------HVVANISAP----GQLRWGDSYANALKAN 116

Qy        177 ALEEKENKILVKETGYFFIYGQVLY-----TDKTYAMGHLIQRKKVHVFGDELSLVTLFR 231
               :| |:|:::|   | : || |||:          : | | |  |  :  :::::  :
Db        117 GVELKDNQLVVPTDGLYLIYSQVLFRGHGCPSTPLFLTHTISRIAVS-YQTKVNILSAIK 175

Qy        232 --CIQNMPETLP----NNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKL 284
                | :  ||           |  |: :||:|| |   | :       :    :|| : |
Db        176 SPCHRETPEGAEAKPWYEPIYQGGVFQLEKGDRLSAEINQPEYLDYAESGQVYFGIIAL 234


RESULT 15
TNFA_LAMGL
ID   TNFA_LAMGL     STANDARD;      PRT;   233 AA.
AC   P59694;
DT   15-SEP-2003 (Rel. 42, Created)
DT   15-SEP-2003 (Rel. 42, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin).
GN   TNF OR TNFSF2 OR TNFA.
OS   Lama glama (Llama).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
OX   NCBI_TaxID=9844;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Raadan O., Lee S., Yoshida R., Chang K., Ohashi K., Sugimoto C.,
RA   Onuma M.;
RT   "Cloning and sequence analysis of cytokine cDNAs of llama and camel.";
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation (By similarity).
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
```

```
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form ocurrs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB107646; BAC75383.1; -.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Transmembrane; Signal-anchor; Phosphorylation.
FT   CHAIN         1    233       TUMOR NECROSIS FACTOR, MEMBRANE FORM (BY
FT                                SIMILARITY).
FT   CHAIN        77    233       TUMOR NECROSIS FACTOR, SOLUBLE FORM (BY
FT                                SIMILARITY).
FT   DOMAIN        1     34       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     35     57       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                (BY SIMILARITY).
FT   DOMAIN       58    233       EXTRACELLULAR (POTENTIAL).
FT   MOD_RES       2      2       PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
FT   SITE         76     77       CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT   DISULFID    145    177       BY SIMILARITY.
SQ   SEQUENCE   233 AA;  25437 MW;  F5C07837505FBD86 CRC64;

  Query Match             7.3%;  Score 105.5;  DB 1;  Length 233;
  Best Local Similarity   22.2%;  Pred. No. 0.077;
  Matches   53;  Conservative   34;  Mismatches  101;  Indels   51;  Gaps    8;

Qy         60 CLTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPA 119
              ||:: ||  ||        |   : |   |:|                    ||:|  | |
Db         32 CLSLFSFLLVAGATTLFCLLHFGVIGPQKEEL----------------LTGLQIMNPLA 74

Qy        120 PGEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKR---GS 176
             :||| ||:|       :   |  ||                  |   |      :
Db         75 QTLRSSSQASRDKPVAHVVADPAAQGQLQ----------------WEKRFANTLLAN 115

Qy        177 ALEEKENKILVKETGYFFIYGQVLYTDK-----TYAMGHLIQRKKVHVFGDELSLVTLFR 231
               :: ::|:::|   | : || |||:: :       : | | |  |  : :: :|::  :
Db        116 GVKLEDNQLVVPTDGLYLIYSQVLFSGQRCPSTPVFLTHTISRLAVS-YPNKANLLSAIK 174

Qy        232 --C---IQNMPETLP-NNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKL 284
                 |       | |     |  |: :||: | |   |   |     :    :|| : |
Db        175 SPCQGGTSEEAEAKPWYEPIYLGGVFQLEKDDRLSAEINMPNYLDFAESGQVYFGIIAL 233


Search completed: August 28, 2003, 18:03:55
Job time : 24 secs
```

GenCore version 5.1.6

QM protein - protein search, using sw model

Run on: August 28, 2003, 18:00:21 ; Search time 97 Seconds
(without alignments)
758.196 Million cell updates/sec

Title: US-09-507-968D-2
Perfect score: 1451
Sequence: 1 MDDSTEREQSRLTSCLKKRE.....ENAQISLDGDVTFFGALKLL 285

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1069	73.7	208	4	Q8IZI6	Q8izi6 homo sapien
2	897	61.8	174	4	Q8IZI5	Q8izi5 homo sapien
3	862.5	59.4	258	11	Q8BZM8	Q8bzm8 mus musculu
4	812	56.0	158	4	Q8IZI4	Q8izi4 homo sapien
5	708	48.8	288	13	Q8JHJ4	Q8jhj4 gallus gall
6	339	23.4	199	11	Q8BWP2	Q8bwp2 mus musculu
7	336	23.2	194	11	Q8BVA3	Q8bva3 mus musculu
8	247.5	17.1	410	11	Q8BXS2	Q8bxs2 mus musculu
9	244.5	16.9	250	4	Q8NFH7	Q8nfh7 homo sapien
10	235.5	16.2	330	4	Q8IZK7	Q8izk7 homo sapien
11	112.5	7.8	235	11	Q9JI26	Q9ji26 rattus norv
12	110.5	7.6	235	11	Q9JI27	Q9ji27 rattus norv
13	109	7.5	261	5	Q8MRW2	Q8mrw2 drosophila
14	109	7.5	325	5	Q9V5G2	Q9v5g2 drosophila
15	109	7.5	415	5	Q8MUJ1	Q8muj1 drosophila
16	106.5	7.3	252	11	Q8K3Y8	Q8k3y8 mus musculu
17	104.5	7.2	255	13	Q9DEP9	Q9dep9 oncorhynchu
18	102	7.0	287	13	Q90WT9	Q90wt9 gallus gall
19	102	7.0	409	5	Q8MY88	Q8my88 drosophila
20	101	7.0	409	5	Q8IGD3	Q8igd3 drosophila
21	100.5	6.9	205	4	Q8N4C3	Q8n4c3 homo sapien
22	99.5	6.9	217	6	Q9BEF4	Q9bef4 cabassous u
23	99	6.8	251	4	Q8NFE9	Q8nfe9 homo sapien
24	98	6.8	255	13	Q9I8I0	Q9i8i0 salvelinus
25	97.5	6.7	1596	13	Q9I8E1	Q9i8e1 fugu rubrip
26	97	6.7	217	11	Q9ERG6	Q9erg6 peromyscus
27	95.5	6.6	233	6	Q8MKG8	Q8mkg8 saimiri sci
28	95.5	6.6	252	11	Q8K3Y7	Q8k3y7 rattus norv
29	95	6.5	289	17	Q8TVG6	Q8tvg6 methanopyru
30	94.5	6.5	215	11	Q99ND1	Q99nd1 tamiasciuru
31	94.5	6.5	237	13	Q8AWC9	Q8awc9 cyprinus ca
32	94.5	6.5	246	13	Q9I976	Q9i976 oncorhynchu
33	94.5	6.5	246	13	Q9I970	Q9i970 oncorhynchu
34	94.5	6.5	347	16	Q9RXM2	Q9rxm2 deinococcus
35	94	6.5	1695	5	Q9NK53	Q9nk53 drosophila
36	94	6.5	1711	5	Q9VJL0	Q9vjl0 drosophila
37	94	6.5	1883	4	Q9H2Y7	Q9h2y7 homo sapien
38	93.5	6.4	157	4	O43647	O43647 homo sapien
39	93.5	6.4	214	6	Q9BEF3	Q9bef3 didelphis m
40	93	6.4	596	10	Q9C977	Q9c977 arabidopsis
41	92.5	6.4	149	6	O97543	O97543 aotus nancy
42	92.5	6.4	253	13	Q8JFG3	Q8jfg3 sparus aura
43	92	6.3	1695	5	Q9U9R5	Q9u9r5 drosophila
44	92	6.3	1711	5	Q9U9R4	Q9u9r4 drosophila
45	91.5	6.3	2027	13	Q8UW52	Q8uw52 fugu rubrip

ALIGNMENTS

RESULT 1
Q8IZI6
ID Q8IZI6 PRELIMINARY; PRT; 208 AA.
AC Q8IZI6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE B-lymphocyte stimulator (Fragment).
GN TNFSF13B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Gao H., He F., Li R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY129226; AAN08422.1; -.
FT NON_TER 1 1
SQ SEQUENCE 208 AA; 22767 MW; EEA31D227033AA53 CRC64;

Query Match 73.7%; Score 1069; DB 4; Length 208;
Best Local Similarity 99.5%; Pred. No. 2e-93;
Matches 207; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy         78 SLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAPGEGNSSQNSRNKRAVQG 137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 SLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAPGEGNSSQNSRNKRAVQG 60

Qy        138 PEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEEKENKILVKETGYFFIYG 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEEKENKILVKETGYFFIYG 120

Qy        198 QVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETLPNNSCYSAGIAKLEEGD 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETLPNNSCYSAGIAKLEEGD 180

Qy        258 ELQLAIPRENAQISLDGDVTFFGALKLL 285
              |||| ||||||||||||||||||||||||
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```
Db        181 ELQLTIPRENAQISLDGDVTFFGALKLL 208


RESULT 2
Q8IZI5
ID   Q8IZI5      PRELIMINARY;      PRT;   174 AA.
AC   Q8IZI5;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   B-lymphocyte stimulator (Fragment).
GN   TNFSF13B.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   He F., Gao H., Li R.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY129227; AAN08423.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   174 AA;  19479 MW;  1AEBD4F2862EB3E0 CRC64;

  Query Match             61.8%;  Score 897;  DB 4;  Length 174;
  Best Local Similarity   99.4%;  Pred. No. 3.5e-77;
  Matches  173;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        112 LKIFEPPAPGEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLS 171
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 LKIFEPPAPGEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLS 60

Qy        172 FKRGSALEEKENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFR 231
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FKRGSALEEKENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFR 120

Qy        232 CIQNMPETLPNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CIQNMPETLPNNSCYSAGIAKLEEGDELQLTIPRENAQISLDGDVTFFGALKLL 174


RESULT 3
Q8BZM8
ID   Q8BZM8      PRELIMINARY;      PRT;   258 AA.
AC   Q8BZM8;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Tumor necrosis factor (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK034121; BAC28593.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   258 AA;  28604 MW;  E6431FE93E782810 CRC64;

  Query Match             59.4%;  Score 862.5;  DB 11;  Length 258;
  Best Local Similarity   65.0%;  Pred. No. 1.2e-73;
  Matches  173;  Conservative   24;  Mismatches   30;  Indels   39;  Gaps    2;

Qy         51 TLLLALLSCCLTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTA 110
              ||||||||   | :| ||:|||| || :|| ||| :     || ||||:        :||
Db          1 TLLLALLSSSFTAMSLYQLAALQADLMNLRMELQSYRGSATPAAAGAPE--------LTA 52

Qy        111 GLKIFEPPAPGEGNSSQNSRNKRAVQGPEET---------------------------- 141
              |:|:  | ||   |||:  ||:|| ||||||
Db         53 GVKLLTPAAPRPHNSSRGHRNRRAFQGPEETEQDVDLSAPPAPCLPGCRHSQHDDNGMNL 112

Qy        142 --VTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEEKENKILVKETGYFFIYGQV 199
                : ||||||||||:||||:||:|||||||||||||:|||||||||:|::||||||| ||
Db        113 RNIIQDCLQLIADSDTPTIRKGTYTFVPWLLSFKRGNALEEKENKIVVRQTGYFFIYSQV 172

Qy        200 LYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETLPNNSCYSAGIAKLEEGDEL 259
              ||||  :||||:||||||||||||||||||||||||||:|||||||||||||:||||||
Db        173 LYTDPIFAMGHVIQRKKVHVFGDELSLVTLFRCIQNMPKTLPNNSCYSAGIARLEEGDEI 232

Qy        260 QLAIPRENAQISLDGDVTFFGALKLL 285
              |||||||||||| :|| ||||||||| .
Db        233 QLAIPRENAQISRNGDDTFFGALKLL 258


RESULT 4
Q8IZI4
ID   Q8IZI4      PRELIMINARY;      PRT;   158 AA.
AC   Q8IZI4;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   B-lymphocyte stimulator (Fragment).
GN   TNFSF13B.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   He F., Gao H., Li R.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY129228; AAN08424.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   158 AA;  17826 MW;  8346BCC0D333DCAB CRC64;

  Query Match             56.0%;  Score 812;  DB 4;  Length 158;
  Best Local Similarity   99.4%;  Pred. No. 3.7e-69;
  Matches  157;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        128 NSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEEKENKILV 187
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 NSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEEKENKILV 60

Qy        188 KETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETLPNNSCYS 247
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETLPNNSCYS 120

Qy        248 AGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
              |||||||||||||| ||||||||||||||||||||||
Db        121 AGIAKLEEGDELQLTIPRENAQISLDGDVTFFGALKLL 158


RESULT 5
Q8JHJ4
ID   Q8JHJ4      PRELIMINARY;      PRT;   288 AA.
AC   Q8JHJ4;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   TNF family B cell activation factor.
GN   BAFF.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Schneider K., Kolthow S., Schneider P., Goebel T., Kaspers B.,
```

```
RA   Staeheli P.;
RT   "A chicken homolog of the B cell activating factor of the TNF family
RT   (BAFF).";
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF506010; AAM90951.2; -.
SQ   SEQUENCE   288 AA;  31629 MW;  8E2F291D2495BB79 CRC64;

  Query Match             48.8%;  Score 708;  DB 13;  Length 288;
  Best Local Similarity   52.1%;  Pred. No. 6.7e-59;
  Matches  152;  Conservative   39;  Mismatches   69;  Indels   32;  Gaps    5;

Qy         22 MKLKECVSILPRKESPSVRSSKDGKLLAATLLLA--------LLSCCLTVVSFYQVAALQ 73
              ||  :|| :: :|:: |  |   |     | | :        ||| ||  || |    |:
Db          1 MKSVDCVHVIQQKDTASSPSGPPGAASGTTGLFSVTFLWLAMLLSSCLAAVSLYHAITLK 60

Qy         74 GDLASLRAEL-----QGHHAEKLPAGAGAPKAGLEEAPAVTAGLKI----------FEPP 118
               :| :||:||          |: |   |  |||     :|:: |::             |
Db         61 TELEALRSELIYRVRARSPLEQPPVSPGDKKAG----ASVSSFLQVSAAGARQENRLPGP 116

Qy        119 APGEGNSSQ-----NSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFK 173
              :| |   ::      :| :|::   |||| | ||||||||::   ||   : ||||||||
Db        117 SPAESFQTEIWDRNRNRGRRSIVNAEETVLQACLQLIADSKSDIQQKDDSSIVPWLLSFK 176

Qy        174 RGSALEEKENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCI 233
              ||:|||||: |||::|||||||||||||||| |:|||||||||| |||||:|||||||||
Db        177 RGTALEEQGNKIVIKETGYFFIYGQVLYTDTTFAMGHLIQRKKAHVFGDDLSLVTLFRCI 236

Qy        234 QNMPETLPNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
              ||||:: |||||||:|||||||||||||||| |||  |:|||||| |||||::||
Db        237 QNMPQSYPNNSCYTAGIAKLEEGDELQLTIPRRRAKISLDGDGTFFGAVRLL 288


RESULT 6
Q8BWP2
ID   Q8BWP2      PRELIMINARY;      PRT;   199 AA.
AC   Q8BWP2;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Tumor necrosis factor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Liver;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK050384; BAC34225.1; -.
SQ   SEQUENCE   199 AA;  21654 MW;  39392021D4EFD320 CRC64;

  Query Match             23.4%;  Score 339;  DB 11;  Length 199;
  Best Local Similarity   43.6%;  Pred. No. 4.7e-24;
  Matches   85;  Conservative   22;  Mismatches   46;  Indels   42;  Gaps    5;

Qy          1 MDDSTER-EQSRLTSCLKKREEMKLKECVSILPRKESPS-VRSSKDGKLLAATLLLALLS 58
              ||:| :      |  | :| |:||:     | |:||  :     :||:|||||||||||
Db          1 MDESAKTLPPPCLCFCSEKGEDMKV-GYDPITPQKEEGAWFGICRDGRLLAATLLLALLS 59

Qy         59 CCLTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPP 118
                 | :| ||:|||| || :|| ||| :     || ||||:        :|||:|:  |
Db         60 SSFTAMSLYQLAALQADLMNLRMELQSYRGSATPAAAGAPE--------LTAGVKLLTPA 111

Qy        119 APGEGNSSQNSRNKRAVQGPEET-----------------------------VTQDCL 147
              ||   |||:  ||:|| ||||||                             : ||||
Db        112 APRPHNSSRGHRNRRAFQGPEETEQDVDLSAPPAPCLPGCRHSQHDDNGMNLRNIIQDCL 171

Qy        148 QLIADSETPTIQKGS 162
              |||||:||||:|||
Db        172 QLIADSDTPTIRKGS 186


RESULT 7
Q8BVA3
ID   Q8BVA3      PRELIMINARY;      PRT;   194 AA.
AC   Q8BVA3;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Tumor necrosis factor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK079180; BAC37571.1; -.
SQ   SEQUENCE   194 AA;  20961 MW;  85FCF3495B138377 CRC64;

  Query Match             23.2%;  Score 336;  DB 11;  Length 194;
  Best Local Similarity   43.1%;  Pred. No. 8.8e-24;
  Matches   84;  Conservative   23;  Mismatches   46;  Indels   42;  Gaps    5;

Qy          1 MDDSTER-EQSRLTSCLKKREEMKLKECVSILPRKESPS-VRSSKDGKLLAATLLLALLS 58
              ||:| :      |  | :| |:||:     | |:||  :     :||:|||||||||||
Db          1 MDESAKTLPPPCLCFCSEKGEDMKV-GYDPITPQKEEGAWFGICRDGRLLAATLLLALLS 59

Qy         59 CCLTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPP 118
                 | :| ||:|||| || :|| ||| :     || ||||:        :|||:|:  |
Db         60 SSFTAMSLYQLAALQADLMNLRMELQSYRGSATPAAAGAPE--------LTAGVKLLTPA 111

Qy        119 APGEGNSSQNSRNKRAVQGPEET-----------------------------VTQDCL 147
              ||   |||:  ||:|| ||||||                             : ||||
Db        112 APRPHNSSRGHRNRRAFQGPEETEQDVDLSAPPAPCLPGCRHSQHDDNGMNLRNIIQDCL 171

Qy        148 QLIADSETPTIQKGS 162
              |||||:||||:|||:
Db        172 QLIADSDTPTIRKGN 186


RESULT 8
Q8BXS2
ID   Q8BXS2      PRELIMINARY;      PRT;   410 AA.
AC   Q8BXS2;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Tumor necrosis factor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Retina;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK044387; BAC31897.1; -.
SQ   SEQUENCE   410 AA;  45881 MW;  590A4B74C33FB8D4 CRC64;
```

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  Query Match             17.1%;  Score 247.5;  DB 11;  Length 410;
  Best Local Similarity   31.6%;  Pred. No. 6.7e-15;
  Matches   74;  Conservative   35;  Mismatches   78;  Indels   47;  Gaps    8;

Qy         68 QVAALQGDLASLRAELQGHHAEKLPAGAGAPKAG-------LEEAPAVTAGLKIFEPPAP 120
              |:  | :| ||| |:    :    :|  : | |        |::| |    |
Db        207 QLRLCQTELQSLRREV----SRLQRSGGPSQKQGERPWQSLWEQSPDVLEAWK------- 255

Qy        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLI-------ADSETPTIQKGSYTFVPWLLSFK 173
                  || :|||   :     | |:       |||:          | | |    :
Db        256 ----DGAKSRRRRAVLTQKHKKKHSVLHLVPVNITSKADSDV--------TEVMWQPVLR 303

Qy        174 RGSALEEKENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCI 233
              ||  || : : : | :|| : :| |||: | |: || :: |:       :    ||||||
Db        304 RGRGLEAQGDIVRVWDTGIYLLYSQVLFHDVTFTMGQVVSRE------GQGRRETLFRCI 357

Qy        234 QNMPETLPN---NSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKL 284
              ::||   |:   |||||||:  | :|| : : ||| ||::||    || | :||
Db        358 RSMPSD-PDRAYNSCYSAGVFHLHQGDIITVKIPRANAKLSLSPHGTFLGFVKL 410


RESULT 9
Q8NFH7
ID   Q8NFH7      PRELIMINARY;      PRT;   250 AA.
AC   Q8NFH7;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Proliferation-inducing ligand APRIL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Koyama T., Tsukamoto H., Masumoto K., Himeji D., Hayashi K.,
RA   Harada M., Horiuchi T.;
RT   "Genomic structure of APRIL, a proliferation-inducing ligand.";
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF513501; AAM47279.1; -.
DR   InterPro; IPR006052; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   250 AA;  27453 MW;  AE1E4FDEFD578898 CRC64;

  Query Match             16.9%;  Score 244.5;  DB 4;  Length 250;
  Best Local Similarity   29.7%;  Pred. No. 6.3e-15;
  Matches   70;  Conservative   47;  Mismatches   90;  Indels   29;  Gaps    8;

Qy         54 LALLSCCLTVVSFYQVAALQGDLASLRAELQGHHAEKLPA--GAGAPKAGLEEAPAVTAG 111
              |  ::| : :::       | :| ||| |:        |:  | | |   | |    :
Db         39 LGAVACAMALLT------QQTELQSLRREVSRLQGTGGPSQNGEGYPWQSLPEQS--SDA 90

Qy        112 LKIFEPPAPGEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLS 171
              |: :|        : : || :|||   ::       | |:  : | :       | | |  :
Db         91 LEAWE--------NGERSRKRRAVLTQKQKKQHSVLHLVPINAT-SKDDSDVTEVMWQPA 141

Qy        172 FKRGSALEEKENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFR 231
               :||  |: :   : ::: | : :| |||: | |: || :: |:       :    ||||
Db        142 LRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQVVSRE------GQGRQETLFR 195

Qy        232 CIQNMPETLPN---NSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKL 284
              ||::|| : |:   |||||||:  | :|| | : |||  |:::|    || | :||
Db        196 CIRSMP-SHPDRAYNSCYSAGVFHLHQGDILSVIIPRARAKLNLSPHGTFLGFVKL 250


RESULT 10
Q8IZK7
ID   Q8IZK7      PRELIMINARY;      PRT;   330 AA.
AC   Q8IZK7;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   TWE-PRIL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22299924; PubMed=12411489;
RA   Pradet-Balade B., Medema J.P., Lopez-Fraga M., Lozano J.C.,
RA   Kolfschoten G.M., Picard A., Martinez-A C., Garcia-Sanz J.A.,
RA   Hahne M.;
RT   "An endogenous hybrid mRNA encodes TWE-PRIL, a functional cell surface
RT   TWEAK-APRIL fusion protein.";
RL   EMBO J. 21:5711-5720(2002).
DR   EMBL; AY081051; AAL90443.1; -.
SQ   SEQUENCE   330 AA;  36588 MW;  FC6F3BCA29C029AE CRC64;

  Query Match             16.2%;  Score 235.5;  DB 4;  Length 330;
  Best Local Similarity   26.3%;  Pred. No. 6.7e-14;
  Matches   73;  Conservative   45;  Mismatches  101;  Indels   59;  Gaps    8;

Qy         30 ILPRKESPSVRSSKDGKLLAATLLLALLSCCLTVVSFYQVAALQGDLASLRAELQGHHAE 89
              : ||: :|  | ::  : :||              |:|   |             :
Db         89 VRPRRSAPKGRKTRARRAIAA--------------HYEVHPRPGQ-------------D 120

Qy         90 KLPAGAGAPKAGLEEAP----------------AVTAGLKIF---EPPAPGEGNSSQNS 129
                 ||     :| |||                    |||         |     : : |
Db        121 GAQAGVDGTVSGWEEARINSSSPLRYNRQIGEFIVTRAGLYYLYCQSSDALEAWENGERS 180

Qy        130 RNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEEKENKILVKE 189
              | :|||   ::       | |:  : | :       | | |  : :||  |: :   : :::
Db        181 RKRRAVLTQKQKKQHSVLHLVPINAT-SKDDSDVTEVMWQPALRRGRGLQAQGYGVRIQD 239

Qy        190 TGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETLPN---NSCY 246
              | : :| |||: | |: || :: |:       :    ||||||::|| : |:   ||||
Db        240 AGVYLLYSQVLFQDVTFTMGQVVSRE------GQGRQETLFRCIRSMP-SHPDRAYNSCY 292

Qy        247 SAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKL 284
              |||:  | :|| | : |||  |:::|    || | :||
Db        293 SAGVFHLHQGDILSVIIPRARAKLNLSPHGTFLGFVKL 330


RESULT 11
Q9JI26
ID   Q9JI26      PRELIMINARY;      PRT;   235 AA.
AC   Q9JI26;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   TNF-alpha propeptide 3 (Fragment).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Dark Agouti;
RA   Seidel M.F., Junier M.-P., Vetter H.;
RT   "TNF-alpha polymorphism in rats with collagen-induced arthritis.";
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF269160; AAF82568.1; -.
DR   HSSP; P06804; 2TNF.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
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FT   NON_TER     235    235
SQ   SEQUENCE   235 AA;  25789 MW;  C801B92D049C2F2E CRC64;

  Query Match             7.8%;  Score 112.5;  DB 11;  Length 235;
  Best Local Similarity   22.2%;  Pred. No. 0.02;
  Matches   54;  Conservative   45;  Mismatches   87;  Indels   57;  Gaps   11;

Qy         60 CLTVVSFYQVAALQGDLASLRAELQG-HHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPP 118
              ||:: ||  ||        |   : | :  || | |       |  : | |  |:
Db         32 CLSLFSFLLVAGATTLFCLLNFGVIGPNKEEKFPNG-----LPLISSMAQTLTLR----- 81

Qy        119 APGEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSAL 178
                   :|||||  :|          :: |: ::      :  |               :
Db         82 -----SSSQNSSDKPVAHVVANHQAEEQLEWLSQRANALLANG---------------M 120

Qy        179 EEKENKILVKETGYFFIYGQVLYTDK----TYAMGHLIQRKKVHVFGDELSLVTLFR--C 232
             : |:|:::|   | : || |||:  :       : | : |  :  : :::||::  :  |
Db        121 DPKDNQLVVPADGLYLIYSQVLFKGQGCPDYVLLTHTVSRFAIS-YQEKVSLLSAIKSPC 179

Qy        233 IQNMPETLP----NNSCYSAGIAKLEEGDELQLAIPRENAQISLDG--DVT-----FFGA 281
              :: ||          |  |: :||:|| |       :|:::|    |:|     :||
Db        180 PKDTPEGAELKPWYEPMYLGGVFQLEKGDLL-------SAEVNLPKYLDITESGQVYFGV 232

Qy        282 LKL 284
             : |
Db        233 IAL 235


RESULT 12
Q9JI27
ID   Q9JI27      PRELIMINARY;      PRT;   235 AA.
AC   Q9JI27;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   TNF-alpha propeptide 5 (Fragment).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Dark Agouti;
RA   Seidel M.F., Junier M.-P., Vetter H.;
RT   "TNF-alpha polymorphism in rats with collagen-induced arthritis.";
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF269159; AAF82567.1; -.
DR   HSSP; P06804; 2TNF.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER     235    235
SQ   SEQUENCE   235 AA;  25806 MW;  12A8EC6D0491428D CRC64;

  Query Match             7.6%;  Score 110.5;  DB 11;  Length 235;
  Best Local Similarity   22.2%;  Pred. No. 0.032;
  Matches   54;  Conservative   45;  Mismatches   87;  Indels   57;  Gaps   11;

Qy         60 CLTVVSFYQVAALQGDLASLRAELQG-HHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPP 118
              ||:: ||  ||        |   : | :  || | |       |  : | |  |:
Db         32 CLSLFSFLLVAGATTLFCLLNFGVIGPNKEEKFPNG-----LPLISSMAQTLTLR----- 81

Qy        119 APGEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSAL 178
                   :|||||  :|          :: |: ::      :  |               :
Db         82 -----SSSQNSSDKPVAHVVANHQAEEQLEWLSQRANALLANG---------------M 120

Qy        179 EEKENKILVKETGYFFIYGQVLYTDK----TYAMGHLIQRKKVHVFGDELSLVTLFR--C 232
             : |:|:::|   | : || |||:  :       : | : |  :  : :::||::  :  |
Db        121 DPKDNQLVVPADGLYLIYSQVLFKGQGCPDYVLLTHTVSRFAIS-YQEKVSLLSAIKSPC 179

Qy        233 IQNMPETLP----NNSCYSAGIAKLEEGDELQLAIPRENAQISLDG--DVT-----FFGA 281
              :: ||          |  |: :||:|| |       :|:::|    |:|     :||
Db        180 PKDTPEGAELKPWYEPMYLGGVFQLEKGDLL-------SAEVNLPKYLDITESGQVYFGV 232

Qy        282 LKL 284
             : |
Db        233 IAL 235


RESULT 13
Q8MRW2
ID   Q8MRW2      PRELIMINARY;      PRT;   261 AA.
AC   Q8MRW2;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   SD18286p.
GN   EIGER OR CG12919.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA   Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA   George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA   Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA   Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA   Celniker S.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY119233; AAM51093.1; -.
DR   FlyBase; FBgn0033483; eiger.
DR   InterPro; IPR006052; TNF_family.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   261 AA;  29780 MW;  13B6D5A04EC9122C CRC64;

  Query Match             7.5%;  Score 109;  DB 5;  Length 261;
  Best Local Similarity   20.9%;  Pred. No. 0.051;
  Matches   50;  Conservative   44;  Mismatches   79;  Indels   66;  Gaps   11;

Qy         76 LASLRAE---LQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAPGEGNSSQNSRNK 132
              :| :| |   :||:| |           |:|  :  |  |  | |||       :||::
Db         59 IADVRNEEQNIQGNHTE-----------LQEKSSNEATSK--ESPAPLHHRRRRMHSRHR 104

Qy        133 RAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKR---GSA----------- 177
                 :    |::      | | ||       |     : || :|   ||
Db        105 HLLVRKGESL------LSARSE------DSRPAAHFHLSSRRRHQGSMGYHGDMYIGNDN 152

Qy        178 --------LEEKENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTL 229
                      : ::  : |  || :::| |: | :     | :: :      ||
Db        153 ERNSYQGHFQTRDGVLTVTNTGLYYVYAQICYNNSHDQNGFIVFQ------GD----TPF 202

Qy        230 FRCIQNMPETLPN--NSCYSAGIAKLEEGDELQLAIPR--ENAQISLDGDVTFFGALKL 284
              :|:  :|  :|:  ::|:::|:  ||  : : |       || :    : ::||  |:
Db        203 LQCLNTVPTNMPHKVHTCHTSGLIHLERNERIHLKDIHNDRNAVLREGNNRSYFGIFKV 261


RESULT 14
Q9V5G2
ID   Q9V5G2      PRELIMINARY;      PRT;   325 AA.
AC   Q9V5G2;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   CG12919 protein.
GN   EIGER OR CG12919.
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OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BERKELEY;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
DR   EMBL; AE003831; AAF58848.1; -.
DR   FlyBase; FBgn0033483; eiger.
DR   InterPro; IPR006052; TNF_family.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   325 AA;  36862 MW;  6E5CCB69694F1A3A CRC64;

  Query Match             7.5%;  Score 109;  DB 5;  Length 325;
  Best Local Similarity   20.9%;  Pred. No. 0.07;
  Matches   50;  Conservative   44;  Mismatches   79;  Indels   66;  Gaps   11;

Qy         76 LASLRAE---LQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAPGEGNSSQNSRNK 132
              :| :| |   :||:| |            |:|  :  |  |  | |||       :||::
Db        123 IADVRNEEQNIQGNHTE-----------LQEKSSNEATSK--ESPAPLHHRRRMHSRHR 168

Qy        133 RAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKR---GSA----------- 177
                :    |::      | | ||       |     : || :|   ||
Db        169 HLLVRKGESL------LSARSE------DSRPAAHFHLSSRRRHQGSMGYHGDMYIGNDN 216

Qy        178 --------LEEKENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTL 229
                      : ::  : |  || :::| |: | :     | :: :      ||
Db        217 ERNSYQGHFQTRDGVLTVTNTGLYYVYAQICYNNSHDQNGFIVFQ------GD----TPF 266

Qy        230 FRCIQNMPETLPN--NSCYSAGIAKLEEGDELQLAIPR--ENAQISLDGDVTFFGALKL 284
               :|:  :|  :|:  ::|:::|:  ||  : : |       || :    : ::||  |:
Db        267 LQCLNTVPTNMPHKVHTCHTSGLIHLERNERIHLKDIHNDRNAVLREGNNRSYFGIFKV 325


RESULT 15
Q8MUJ1
ID   Q8MUJ1      PRELIMINARY;      PRT;   415 AA.
AC   Q8MUJ1;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Eiger.
GN   EIGER OR CG12919.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22165923; PubMed=12176339;
RA   Moreno E., Yan M., Basler K.;
RT   "Evolution of TNF Signaling Mechanisms. JNK-Dependent Apoptosis
RT   Triggered by Eiger, the Drosophila Homolog of the TNF Superfamily.";
RL   Curr. Biol. 12:1263-1268(2002).
DR   EMBL; AF521176; AAM76710.1; -.
DR   FlyBase; FBgn0033483; eiger.
DR   InterPro; IPR006052; TNF_family.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   415 AA;  46918 MW;  E087A26DE222D2BF CRC64;

  Query Match             7.5%;  Score 109;  DB 5;  Length 415;
  Best Local Similarity   20.9%;  Pred. No. 0.099;
  Matches   50;  Conservative   44;  Mismatches   79;  Indels   66;  Gaps   11;

Qy         76 LASLRAE---LQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAPGEGNSSQNSRNK 132
              :| :| |   :||:| |            |:|  :  |  |  | |||       :||::
Db        213 IADVRNEEQNIQGNHTE-----------LQEKSSNEATSK--ESPAPLHHRRRMHSRHR 258

Qy        133 RAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKR---GSA----------- 177
                :    |::      | | ||       |     : || :|   ||
Db        259 HLLVRKGESL------LSARSE------DSRPAAHFHLSSRRRHQGSMGYHGDMYIGNDN 306

Qy        178 --------LEEKENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTL 229
                      : ::  : |  || :::| |: | :     | :: :      ||
Db        307 ERNSYQGHFQTRDGVLTVTNTGLYYVYAQICYNNSHDQNGFIVFQ------GD----TPF 356

Qy        230 FRCIQNMPETLPN--NSCYSAGIAKLEEGDELQLAIPR--ENAQISLDGDVTFFGALKL 284
               :|:  :|  :|:  ::|:::|:  ||  : : |       || :    : ::||  |:
Db        357 LQCLNTVPTNMPHKVHTCHTSGLIHLERNERIHLKDIHNDRNAVLREGNNRSYFGIFKV 415


Search completed: August 28, 2003, 18:05:39
Job time : 98 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 28, 2003, 17:53:21 ; Search time 86 Seconds
(without alignments)
526.012 Million cell updates/sec

Title: US-09-507-968D-2
Perfect score: 1451
Sequence: 1 MDDSTEREQSRLTSCLKKRE.....ENAQISLDGDVTFFGALKLL 285

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:*
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2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
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23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1451	100.0	285	19	AAW73043	Tumour necrosis fa
2	1451	100.0	285	19	AAW62461	Human T cell surfa
3	1451	100.0	285	19	AAW58391	Homo sapiens neutr
4	1451	100.0	285	20	AAY22221	Human TNFL1 protei
5	1451	100.0	285	20	AAY04392	Human Kay-ligand.
6	1451	100.0	285	20	AAW93586	Human TNRL1-alpha
7	1451	100.0	285	21	AAB28553	Human TNFL1. Homo
8	1451	100.0	285	21	AAB08659	Amino acid sequenc
9	1451	100.0	285	21	AAB08191	Amino acid sequenc
10	1451	100.0	285	21	AAB08261	Amino acid sequenc
11	1451	100.0	285	22	AAE09242	Human TALL-1 prote
12	1451	100.0	285	22	AAE07156	Human tumour necro
13	1451	100.0	285	22	AAE07879	Human BAFF protein
14	1451	100.0	285	22	AAU12183	Human PRO738 polyp
15	1451	100.0	285	22	AAY71915	Human TACI-ligand
16	1451	100.0	285	22	AAY71978	Human TNF and ApoL
17	1451	100.0	285	23	AAE28963	Human ZTN4 protein
18	1451	100.0	285	23	ABG96458	Human Neutrokine-a
19	1451	100.0	285	23	AAE26214	Human neutrokine-a
20	1451	100.0	285	23	AAE24636	Human tumour necro
21	1451	100.0	285	23	ABB81485	Human ZTNF4 amino
22	1451	100.0	285	23	ABJ00715	Human B lymphocyte
23	1451	100.0	285	23	ABP47217	Human BLyS binding
24	1451	100.0	285	23	ABB95471	Human angiogenesis
25	1451	100.0	285	23	ABG33576	Human B Lymphocyte
26	1451	100.0	285	23	AAU79140	Human Neutrokine-a
27	1451	100.0	285	23	ABB90325	Human polypeptide
28	1451	100.0	285	23	ABB84865	Human PRO738 prote
29	1451	100.0	285	23	AAU75409	Neutrokine-alpha (
30	1451	100.0	285	23	AAU10942	Human AGP-3. Homo
31	1451	100.0	285	24	ABU66581	Human PRO polypept
32	1451	100.0	285	24	ABU66857	Human secreted/tra
33	1451	100.0	285	24	AAE35212	Human tumour necro
34	1451	100.0	285	24	ABP97718	Amino acid sequenc
35	1451	100.0	285	24	ABU59662	Novel secreted and
36	1451	100.0	285	24	ABP57103	Membrane bound BLy
37	1451	100.0	285	24	ABP60543	Human tumour necro
38	1444	99.5	285	21	AAY97037	Membrane bound hum
39	1345	92.7	264	20	AAW82268	Human NTN-2 protei
40	1345	92.7	264	20	AAW82270	Human NTN-2 DNA se
41	1345	92.7	264	21	AAY94005	A human ztnf4, a t
42	1335.5	92.0	266	19	AAW62462	Human T cell surfa
43	1335.5	92.0	266	21	AAB08660	A human neutrokine
44	1335.5	92.0	266	23	ABG96463	Human Neutrokine-a
45	1335.5	92.0	266	23	AAE26215	Human neutrokine-a

ALIGNMENTS

RESULT 1
AAW73043
ID AAW73043 standard; Protein; 285 AA.
XX
AC AAW73043;
XX
DT 07-JAN-1999 (first entry)
XX
DE Tumour necrosis factor homologue TL5 protein.
XX
KW Tumour necrosis factor homologue TL5; vaccine; chronic;
KW acute inflammation; arthritis; septicemia; autoimmune disease;
KW inflammatory bowel disease; psoriasis; transplant rejection;
KW graft vs. host disease; infection; stroke; ischaemia;
KW acute respirator disease syndrome; restenosis; brain injury; AIDS;
KW bone disease; cancer; lymphoproliferative disorder; atherosclerosis;
KW Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN EP869180-A1.
XX
PD 07-OCT-1998.
XX
PF 01-APR-1998; 98EP-0302526.
XX
PR 03-DEC-1997; 97US-0984396.
PR 02-APR-1997; 97US-0041797.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Hurle MR, Young PR;

```
XX
DR   WPI; 1998-508494/44.
DR   N-PSDB; AAV58894.
XX
PT   New tumour necrosis factor homologue, TL5 - useful for diagnosis and
PT   treatment of Alzheimer's disease, AIDS and cancer
XX
PS   Claim 10; Page 18; 23pp; English.
XX
CC   The present sequence encodes a tumour necrosis factor homologue TL5
CC   polypeptide sequence. TL5 polypeptides and antibodies are useful for
CC   identifying compounds which agonise and antagonise TL5, and these can be
CC   administered for treatment to inhibit TL5 activity (antagonist) or
CC   enhance TL5 activity (agonist). Gene therapy using the expression system
CC   can also be used to enhance TL5 activity. Diseases or susceptibility to a
CC   disease can be diagnosed by determining the presence or absence of a
CC   mutation in the TL5 protein. TL5 polynucleotides are useful for locating
CC   genes associated with disease by hybridisation to chromosomes. TL5
CC   polypeptides and polynucleotides can be used, especially to raise an
CC   immune response (i.e. as vaccines) for the treatment of chronic and acute
CC   inflammation, arthritis, septicemia, autoimmune diseases (e.g.
CC   inflammatory bowel disease, psoriasis), transplant rejection,
CC   graft vs. host disease, infection, stroke, ischaemia, acute respiratory
CC   disease syndrome, restenosis, brain injury, AIDS, bone diseases, cancer
CC   (e.g. lymphoproliferative disorders), atherosclerosis, and Alzheimers
CC   disease.
XX
SQ   Sequence   285 AA;

  Query Match             100.0%;  Score 1451;  DB 19;  Length 285;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-145;
  Matches  285;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60

Qy         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120

Qy        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180

Qy        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240

Qy        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
              |||||||||||||||||||||||||||||||||||||||||||||
Db        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285


RESULT 2
AAW62461
ID   AAW62461 standard; Protein; 285 AA.
XX
AC   AAW62461;
XX
DT   05-OCT-1998  (first entry)
XX
DE   Human T cell surface antigen 63954 protein sequence #2.
XX
KW   Human; 63954; primate; rodent; mouse; T cell surface antigen; mammal;
KW   diagnosis; antigen-specific proliferation; cytokine production;
KW   immune response; autoimmune disorder; rheumatoid arthritis;
KW   systemic lupus erythematosis; Hashimoto's autoimmune thyroiditis.
XX
OS   Homo sapiens.
XX
PN   WO9827114-A2.
XX
PD   25-JUN-1998.
XX
PF   16-DEC-1997;   97WO-US23321.
XX
PR   17-DEC-1996;   96US-0033601.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Gorman DM;
XX
DR   WPI; 1998-362719/31.
DR   N-PSDB; AAV39985.
XX
PT   New isolated polypeptide, 63954 - used to develop products for
PT   treating e.g. autoimmune disorders, inflammation, tissue rejection,
PT   cancer or degenerative conditions
XX
PS   Claim 1; Page 60-61; 69pp; English.
XX
CC   The present sequence is a human T cell surface antigen, designated
CC   63954. The novel protein designated 63954 is expressed on T cells.
CC   Protein 63954 can modulate antigen-specific proliferation and cytokine
CC   production on effector cells and may potentiate immune cell expansion or
CC   apoptosis. 63954 agonists or antagonists may also act as a co-stimulatory
CC   molecule for regulation of T cell mediated cell activation, and may cause
CC   a shift of T helper cell types, e.g. between Th1 and Th2. Antagonists of
CC   63954 can be used to modulate immune responses in abnormal situations,
CC   e.g. autoimmune disorders, including rheumatoid arthritis, systemic
CC   lupus erythematosis (SLE), Hashimoto's autoimmune thyroiditis, as well
CC   as acute and chronic inflammatory responses in which T cell activation,
CC   expansion, and/or immunological T cell memory play an important role,
CC   such as chronic inflammation or tissue rejection. The products can also
CC   be used in the treatment of conditions associated with abnormal
CC   physiology or development, including abnormal proliferation, e.g.
CC   cancerous conditions, or degenerative conditions. The products can also
CC   be used for detection, diagnosis and drug screening.
XX
SQ   Sequence   285 AA;

  Query Match             100.0%;  Score 1451;  DB 19;  Length 285;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-145;
  Matches  285;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60

Qy         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120

Qy        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180

Qy        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240

Qy        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
              |||||||||||||||||||||||||||||||||||||||||||||
Db        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285


RESULT 3
AAW58391
ID   AAW58391 standard; Protein; 285 AA.
XX
AC   AAW58391;
XX
DT   11-SEP-1998  (first entry)
XX
DE   Homo sapiens neutrokine alpha protein.
```

```
XX
KW   neutrokine alpha; cell proliferation; differentiation; migration;
KW   cytotoxicity;cell death; treatment; tumour; infection; inflammation;
KW   wound healing; immunodeficiency; autoimmune disease; graft rejection;
KW   fibrotic disorder; haematopoiesis; sepsis; shock; malaria; HIV; AIDS;
KW   acquired immune deficiency syndrome; rheumatoid arthritis; silicosis;
KW   cachexia; detection; diagnosis; drug screening.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          1..46
FT                   /note= "intracellular domain"
FT   Domain          47..72
FT                   /note= "transmembrane domain"
FT   Domain          73..285
FT                   /note= "extracellular domain"
XX
PN   WO9818921-A1.
XX
PD   07-MAY-1998.
XX
PF   25-OCT-1996;   96WO-US17957.
XX
PR   25-OCT-1996;   96WO-US17957.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ebner R,  Ni J,  Yu G;
XX
DR   WPI; 1998-272216/24.
DR   N-PSDB; AAV30934.
XX
PT   New isolated human Neutrokine alpha - used to develop products for
PT   diagnosis and treatment of e.g. tumours, infections,
PT   immunodeficiencies or autoimmune diseases
XX
PS   Claim 17; Fig 1; 104pp; English.
XX
CC   The sequence is that of the neutrokine alpha protein.
CC   Neutrokine alpha (NA) polypeptides modulate cell proliferation,
CC   differentiation, migration, cytotoxicity and cell death,
CC   They can be used to treat e.g. tumour and tumour metastasis, infections
CC   by bacteria, viruses and other parasites, immunodeficiencies,
CC   inflammatory diseases, lymphadenopathy, autoimmune diseases, graft
CC   versus host disease and to stimulate peripheral tolerance, destroy some
CC   transformed cell lines, mediate cell activation and proliferation, and
CC   are functionally linked as primary mediators of immune regulation and
CC   inflammatory responses.  Such activity is useful for immune enhancement
CC   or suppression, myeloprotection, stem cell mobilisation, acute and
CC   chronic inflammatory control and treatment of leukaemia.  They can also
CC   be used to stimulate wound healing and to treat fibrotic disorders
CC   including liver cirrhosis, osteoarthritis and pulmonary fibrosis.  They
CC   can also be used to regulate haematopoiesis, by regulating the activation
CC   and differentiation of various haematopoietic progenitor cells, e.g. to
CC   release mature leukocytes from the bone marrow following chemotherapy,
CC   and in stem cell mobilisation.  NA may also be used to treat sepsis.  NA
CC   antagonists can be used to prevent septic shock, inflammation, cerebral
CC   malaria, activation of the HIV virus, graft-host rejection, bone
CC   resorption, rheumatoid arthritis and cachexia (wasting or malnutrition).
CC   They can also be used to treat e.g. autoimmune diseases such as multiple
CC   sclerosis and insulin-dependent diabetes and inflammatory and infectious
CC   diseases such as silicosis, and sarcoidosis, idiopathic pulmonary
CC   fibrosis, idiopathic hyper-eosinophilic syndrome, endotoxic shock,
CC   atherosclerosis, histamine-mediated allergic reactions and immunological
CC   disorders including late phase allergic reactions, chronic urticaria, and
CC   atopic dermatitis by inhibiting chemokine-induced mast cell and basophil
CC   degranulation and release of histamine.  IgE-mediated allergic reactions
CC   such as allergic asthma, rhinitis and eczema, inflammatory pulmonary
CC   diseases, rheumatoid arthritis, inflammation, degenerative and
CC   inflammatory arthropathies, aplastic anaemia, myelodysplastic syndrome,
CC   subepithelial basement membrane fibrosis or adult respiratory distress
CC   syndrome. The products can also be used for detection, diagnosis and
CC   drug screening.
XX
SQ   Sequence   285 AA;

  Query Match             100.0%;  Score 1451;  DB 19;  Length 285;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-145;
  Matches  285;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60

Qy         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120

Qy        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180

Qy        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240

Qy        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
              |||||||||||||||||||||||||||||||||||||||||||||
Db        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285


RESULT 4
AAY22221
ID   AAY22221 standard; Protein; 285 AA.
XX
AC   AAY22221;
XX
DT   16-SEP-1999  (first entry)
XX
DE   Human TNFL1 protein sequence.
XX
KW   TNFL1; human; TNFR superfamily; tumour necrosis factor ligand; TNF;
KW   tumour necrosis factor receptor; TNFR superfamily; cell proliferation;
KW   cell differentiation; cytokine production; immunoglobulin; hyperplasia;
KW   apoptosis inducer; activated T cell; autoimmune disease; inhibitor;
KW   myasthenia gravis; insulin-dependent diabetes mellitus; endotoxic shock;
KW   rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus;
KW   tumour; proliferative disorder; neoplasia; dysplasia; immunocompetence;
KW   lymphoid organogenesis; bacterial resistance; contact hypersensitivity;
KW   delayed type sensitivity; therapy.
XX
OS   Homo sapiens.
XX
PN   WO9933980-A2.
XX
PD   08-JUL-1999.
XX
PF   22-DEC-1998;   98WO-US27474.
XX
PR   16-DEC-1998;   98US-0212270.
PR   30-DEC-1997;   97US-0068959.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Kassam A,  Lamson G,  Pot D,  Tribouley C;
XX
DR   WPI; 1999-405508/34.
DR   N-PSDB; AAX84620.
XX
PT   New tumour necrosis factor ligands, useful for induction of cell
PT   death and/or proliferation of cells
XX
PS   Claim 1; Page 61; 69pp; English.
XX
CC   This sequence is the tumour necrosis factor (TNF) ligand family
```

CC protein of the invention, designated TNFL1. The TNFL proteins play
CC regulatory roles in cell proliferation and/or differentiation, e.g. they
CC can induce production of cytokines, immunoglobulins, etc. A variety of
CC diseases can be treated by modulating the activity of TNFL proteins,
CC e.g. they can induce apoptosis of activated T cells but rescue resting
CC T cell from apoptosis. TNFL polypeptides can therefore be used to treat
CC autoimmune diseases, such as myasthenia gravis, insulin-dependent
CC diabetes mellitus, rheumatoid arthritis, multiple sclerosis, and systemic
CC lupus erythematosus. TNFL proteins also have tumour stimulating
CC properties, so tumours can be treated by inhibiting the expression or
CC activity of TNFL. Other proliferative disorders, such as neoplasias,
CC dysplasias, and hyperplasia can also be treated using TNFL inhibitors.
CC The TNFL polypeptides and polynucleotides can also be used to enhance or
CC decrease TNF activity, thus providing therapeutic benefits such as
CC induction of cell death, lymphoid organogenesis, or host bacterial
CC resistance, and inhibition of endotoxic shock, contact hypersensitivity,
CC delayed type sensitivity or immunocompetence of a transplant recipient.
CC Tumour necrosis factor (TNF) and its receptors play a major role in host
CC defence and immunosurveillance. As such, there is a need to identify new
CC members of TNFR families. This invention provides this need.
XX
SQ Sequence 285 AA;

Query Match 100.0%; Score 1451; DB 20; Length 285;
Best Local Similarity 100.0%; Pred. No. 4.4e-145;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60

Qy         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120

Qy        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180

Qy        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240

Qy        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
              |||||||||||||||||||||||||||||||||||||||||||||
Db        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
```

RESULT 5
AAY04392
ID AAY04392 standard; Protein; 285 AA.
XX
AC AAY04392;
XX
DT 24-JUN-1999 (first entry)
XX
DE Human Kay-ligand.
XX
KW Kay-ligand; tumour necrosis factor family; TNF; immune system;
KW cytokine; autoimmune disease; tissue graft; cancer; cell death.
XX
OS Homo sapiens.
XX
PN WO9912964-A2.
XX
PD 18-MAR-1999.
XX
PF 11-SEP-1998; 98WO-US19037.
XX
PR 12-SEP-1997; 97US-0058786.
XX
PA (BIOJ) BIOGEN INC.
XX
PI Tschopp J;
XX
DR WPI; 1999-243715/20.
DR N-PSDB; AAX33330.
XX
PT New human or murine Kay-ligands, members of the tumour necrosis
PT factor family
XX
PS Claim 12; Page 32; 41pp; English.
XX
CC The present sequence represents human Kay-ligand, which is a member of
CC the tumour necrosis factor (TNF) family of cytokines. Pharmaceutical
CC compositions containing the Kay-ligand can be used to suppress or
CC stimulate the immune system, especially to prevent or reduce the
CC severity of autoimmune diseases or response to a tissue graft or to
CC treat cancer. An agent capable of interfering with the Kay-ligand can be
CC used to induce cell death. The Kay-ligand can also be used to identify
CC its receptors.
XX
SQ Sequence 285 AA;

Query Match 100.0%; Score 1451; DB 20; Length 285;
Best Local Similarity 100.0%; Pred. No. 4.4e-145;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60

Qy         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120

Qy        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180

Qy        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240

Qy        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
              |||||||||||||||||||||||||||||||||||||||||||||
Db        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
```

RESULT 6
AAW93586
ID AAW93586 standard; Protein; 285 AA.
XX
AC AAW93586;
XX
DT 18-JUN-1999 (first entry)
XX
DE Human TNRL1-alpha protein.
XX
KW Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
KW developmental abnormality; gestational abnormalitity; prostate cancer;
KW APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
KW cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
KW apoptosis; human; TNRL1-alpha.
XX
OS Homo sapiens.
XX
PN WO9911791-A2.
XX
PD 11-MAR-1999.
XX
PF 04-SEP-1998; 98WO-US18393.
XX
PR 05-SEP-1997; 97US-0924634.
XX
PA (UNIW) UNIV WASHINGTON.

```
XX
PI   Chaudhary PM;
XX
DR   WPI; 1999-205191/17.
DR   N-PSDB; AAX23420.
XX
PT   New Tumor Necrosis Factor family receptor polypeptides and ligands -
PT   useful for diagnosis and treatment of prostate cancer and
PT   developmental or gestational abnormalities
XX
PS   Claim 34; Fig 11A; 156pp; English.
XX
CC   This invention describes isolated Tumor Necrosis Factor (TNF) family
CC   receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
CC   fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
CC   their active fragments. APO4 is useful for diagnosing prostate cancer
CC   by determining levels of APO4 in an individual. Prostate cancer can also
CC   be treated using APO4 selective binding agents linked to a therapeutic
CC   moiety. APO4 polypeptides are also useful for identifying selective
CC   binding agents, useful in diagnosis/treatment of disease by binding of
CC   agents to the polypeptide/active fragment which is extracellular, or
CC   expressed on the cell surface. The binding is preferably performed in
CC   vivo. APO4 polypeptides/ active fragments are also useful for screening
CC   for agonists and antagonists by binding and observing the changer in APO4
CC   activity. Effective pharmacological agents useful in diagnosis or
CC   treatment of disease are also identified using APO4 polypeptides/active
CC   fragments and APO4 signal transducer molecules that specifically interact
CC   with a cytoplasmic domain of APO4 and detecting a change in level of APO4
CC   activity. The method is performed in vivo or in vitro. APO polypeptides
CC   are all useful as immunogens for preparing antibodies. APO4 is also
CC   useful for diagnosis/treatment of developmental or gestational
CC   abnormalities. APO8 was transfected to human breast carcinoma cell line
CC   MCF-7, and induced apoptosis.
XX
SQ   Sequence   285 AA;

  Query Match           100.0%;  Score 1451;  DB 20;  Length 285;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-145;
  Matches  285;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60

Qy         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120

Qy        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180

Qy        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240

Qy        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
              |||||||||||||||||||||||||||||||||||||||||||||
Db        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285


RESULT 7
AAB28553
ID   AAB28553 standard; protein; 285 AA.
XX
AC   AAB28553;
XX
DT   08-FEB-2001  (first entry)
XX
DE   Human TNFL1.
XX
KW   Human; tumour necrosis factor like-1; TNFL1; tumour necrosis factor; TNF;
KW   immunosuppressive; antiarthritic; neuroprotective; dermatalogical;
KW   antiinflammatory; antidiabetic; cytostatic; osteopathic; gene therapy;
KW   colon cancer; rheumatoid arthritis; septic shock; Crohn's disease;
KW   osteoporosis; autoimmune disease; myasthenia gravis;
KW   insulin-dependent diabetes mellitus.
XX
OS   Homo sapiens.
XX
PN   WO200060079-A2.
XX
PD   12-OCT-2000.
XX
PF   05-APR-2000; 2000WO-US09058.
XX
PR   05-APR-1999;   99US-0286529.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Tribouley C;
XX
DR   WPI; 2000-665004/64.
DR   N-PSDB; AAC63756.
XX
PT   Tumor necrosis factor (TNF) and TNF receptor superfamily protein
PT   members TNF-L and TNFR-L, useful for enhancing or decreasing TNF
PT   activities such as inducing cell death and lymphoid organogenesis  -
XX
PS   Claim 1; Page 65; 77pp; English.
XX
CC   The present sequence is given in a specification relating to an isolated
CC   human protein designated tumour necrosis factor like-1 (TNFL1). It may be
CC   used to induce cell death in tumours, to induce apoptosis of activated T
CC   cells, to induce inflammation, and to rescue resting T cells from
CC   apoptosis. TNF receptors are used to regulate the function of a TNF
CC   ligand which plays a role in apoptosis, inflammation, differentiation, or
CC   proliferation. Expression of the receptors can also be useful as markers
CC   for cancer, especially for colon cancer. Diseases which can be treated
CC   using ligands and/or receptors of the TNF/TNFR superfamily include
CC   rheumatoid arthritis, cancer, septic shock, Crohn's disease and
CC   osteoporosis. The polynucleotides can be used in gene delivery vehicles,
CC   for the purpose of delivering a mRNA or oligonucleotide, full-length
CC   protein, fusion protein, polypeptide, or ribozyme, or single-chain
CC   antibody, into a cell. The newly identified receptor proteins play
CC   regulatory roles in cell proliferation and/or differentiation. The
CC   receptors can also play a role in the negative regulation of
CC   osteoclastogenesis. Soluble TNFR-like receptors can be useful in the
CC   neutralisation of TNF or TNF-like ligands. A TNF-L protein can also be
CC   used to treat autoimmune diseases (myasthenia gravis and
CC   insulin-dependent diabetes mellitus), tumours, and proliferative
CC   disorders. A TNF-L or TNFR-L subgenomic polynucleotide can also be
CC   delivered to subjects for the purpose of screening test compounds for
CC   those which are useful for enhancing transfer of TNF-L subgenomic
CC   polynucleotides to the cell or for enhancing subsequent biological
CC   effects of TNF-L or TNFR-L subgenomic polynucleotides within the cell.
XX
SQ   Sequence   285 AA;

  Query Match           100.0%;  Score 1451;  DB 21;  Length 285;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-145;
  Matches  285;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60

Qy         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120

Qy        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180

Qy        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240
```

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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240

Qy        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
              |||||||||||||||||||||||||||||||||||||||||||||
Db        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285


RESULT 8
AAB08659
ID   AAB08659 standard; Protein; 285 AA.
XX
AC   AAB08659;
XX
DT   02-JAN-2001  (first entry)
XX
DE   Amino acid sequence of a human neutrokine-alpha polypeptide.
XX
KW   Human; neutrokine-alpha; tumor; tumor metastasis; infection;
KW   immunodeficiency; inflammatory disease; lymphadenopathy;  dermatitis;
KW   autoimmune disease; graft versus host disease; immune regulation;
KW   severe combined immunodeficiency-X-linked agammaglobulinemia;
KW   kappa chain deficiency; B cell lymphoproliferative disorder; purpura;
KW   Wiskott-Aldrich syndrome; systemic lupus erhythematosus; myocarditis;
KW   idiopathic thrombocytopenia purpura; hemolytic anemia; neuritis;
KW   allergic encephalomyelitis; relapsing polychondritis; glomerulonephritis;
KW   rheumatic heart disease; multiple sclerosis; uveitis opthalmia;
KW   polyendocrinopathy; Reiter's disease; autoimmune pulmonary inflammation;
KW   myeloprotection; stem cell mobilization; leukemia.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          1..46
FT                   /note= "intracellular domain"
FT   Domain          47..72
FT                   /note= "transmembrane domain"
FT   Domain          73..285
FT                   /note= "extracellular domain"
FT   Modified-site   124..127
FT                   /note= "potential N-linked glycosylation site"
FT   Modified-site   242..245
FT                   /note= "potential N-linked glycosylation site"
XX
PN   WO200050597-A2.
XX
PD   31-AUG-2000.
XX
PF   22-FEB-2000; 2000WO-US04336.
XX
PR   23-FEB-1999;   99US-0255794.
PR   02-MAR-1999;   99US-0122388.
PR   12-MAR-1999;   99US-0124097.
PR   26-MAR-1999;   99US-0126599.
PR   02-APR-1999;   99US-0127598.
PR   16-APR-1999;   99US-0130412.
PR   23-APR-1999;   99US-0130696.
PR   27-APR-1999;   99US-0131278.
PR   29-APR-1999;   99US-0131673.
PR   28-MAY-1999;   99US-0136784.
PR   06-JUL-1999;   99US-0142659.
PR   27-JUL-1999;   99US-0145824.
PR   24-NOV-1999;   99US-0167239.
PR   03-DEC-1999;   99US-0168624.
PR   16-DEC-1999;   99US-0171108.
PR   23-DEC-1999;   99US-0171626.
PR   14-JAN-2000; 2000US-0176015.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Ni J,  Ebner R,  Yu G;
XX
DR   WPI; 2000-572093/53.
DR   N-PSDB; AAA64427.
XX
PT   Novel cytokine neutrokine-alpha, its splicing variant, neutrokine-alpha
PT   SV polypeptides useful for treating tumor, tumor metastasis, microbial
PT   infections, immunodeficiency, inflammatory diseases, lymphoadenopathy
PT   -
XX
PS   Claim 18; Fig 1A-B; 414pp; English.
XX
CC   The present sequence represents a human neutrokine-alpha polypeptide.
CC   Neutrokine-alpha polypeptides are used to treat, prevent, prognose and
CC   diagnose tumor and tumor metastasis, infections by bacteria, viruses
CC   and other parasites, immunodeficiencies, inflammatory diseases,
CC   lymphadenopathy, autoimmune diseases, graft versus host disease, to
CC   mediate immune regulation and inflammatory responses. Diseases which
CC   may be treated include severe combined immunodeficiency (SCID)-X-linked
CC   agammaglobulinemia, kappa chain deficiency, B cell lymphoproliferative
CC   disorder (BLPD), Wiskott-Aldrich syndrome, systemic lupus erhythematosus,
CC   idiopathic thrombocytopenia purpura, hemolytic anemia, dermatitis,
CC   allergic encephalomyelitis, myocarditis, relapsing polychondritis,
CC   rheumatic heart disease, glomerulonephritis, multiple sclerosis,
CC   Neuritis, Uveitis Opthalmia, Polyendocrinopathies, Purpura
CC   (e.g. Henloch-Scoenlein purpura), Reiter's Disease, and Autoimmune
CC   Pulmonary Inflammation. Neutrokine-alpha is useful for immune
CC   enhancement or suppression, myeloprotection, stem cell mobilization,
CC   acute and chronic inflammatory control and treatment of leukemia.
XX
SQ   Sequence   285 AA;

  Query Match             100.0%;  Score 1451;  DB 21;  Length 285;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-145;
  Matches  285;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60

Qy         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120

Qy        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180

Qy        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240

Qy        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
              |||||||||||||||||||||||||||||||||||||||||||||
Db        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285


RESULT 9
AAB08191
ID   AAB08191 standard; Protein; 285 AA.
XX
AC   AAB08191;
XX
DT   04-DEC-2000  (first entry)
XX
DE   Amino acid sequence of human cytokine designated THANK.
XX
KW   Human; cytokine; THANK; tumour necrosis factor homologue; apoptosis;
KW   nuclear factor-kB; c-jun N-terminal kinase; shock; acute phase response;
KW   viral infection; radiation susceptibility; atherosclerosis; cancer;
KW   acute inflammatory condition; arthritis; allergy;
KW   graft versus host reaction; tumour cell.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
```

```
FT   Domain          1..46
FT                   /note= "intracellular domain"
FT   Domain          47..77
FT                   /note= "transmembrane domain"
FT   Domain          78..111
FT                   /note= "extracellular domain"
FT   Domain          112..285
FT                   /note= "extracellular domain"
XX
PN   WO200045836-A1.
XX
PD   10-AUG-2000.
XX
PF   02-FEB-2000; 2000WO-US02751.
XX
PR   02-FEB-1999;   99US-0118531.
XX
PA   (RERE-) RES DEV FOUND.
XX
PI   Aggarwal BB;
XX
DR   WPI; 2000-514890/46.
XX
PT   Inhibiting the activation of nuclear factor-kB in cells for treating
PT   pathological conditions comprises treating cells with a tumour necrosis
PT   factor homolog inhibitor -
XX
PS   Example 1; Fig 1; 45pp; English.
XX
CC   The present sequence represents a human cytokine, designated THANK.
CC   THANK is a tumour necrosis factor (TNF) homologue that activates
CC   apoptosis, nuclear factor-kB, and c-jun N-terminal kinase. Inhibitors of
CC   the THANK polypeptide are used to inhibit the activation of nuclear
CC   factor-kB in cells. The method is used to inhibit the activation of
CC   nuclear factor-kB in cells, treat pathological conditions such as toxic
CC   and septic shock, acute phase response, viral infection, radiation
CC   susceptibility, atherosclerosis, cancer, acute inflammatory conditions,
CC   arthritis, allergy, and graft versus host reaction, and inhibit growth
CC   of tumour cells such as myeloid cells, colon cancer cells, prostate
CC   cancer cells, cervical carcinoma cells, chronic myeloid leukemic cells
CC   and acute myeloid leukemic cells.
XX
SQ   Sequence   285 AA;

  Query Match             100.0%;  Score 1451;  DB 21;  Length 285;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-145;
  Matches  285;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60

Qy         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120

Qy        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180

Qy        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240

Qy        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
              |||||||||||||||||||||||||||||||||||||||||||||
Db        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285


RESULT 10
AAB08261
ID   AAB08261 standard; Protein; 285 AA.
XX
AC   AAB08261;
XX
DT   04-DEC-2000  (first entry)
XX
DE   Amino acid sequence of a human AGP-3 polypeptide.
XX
KW   AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;
KW   type II transmembrane protein; B cell stimulatory factor;
KW   inflammatory disorder; immune disorder; rheumatoid arthritis;
KW   lupus and graft versus host disease.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          1..46
FT                   /note= "intracellular domain"
FT   Region          42..72
FT                   /note= "transmembrane region"
FT   Domain          73..285
FT                   /note= "extracellular domain"
XX
PN   WO200047740-A2.
XX
PD   17-AUG-2000.
XX
PF   11-FEB-2000; 2000WO-US03653.
XX
PR   12-FEB-1999;   99US-0119906.
PR   18-NOV-1999;   99US-0166271.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Boyle WJ,  Hsu H;
XX
DR   WPI; 2000-558217/51.
DR   N-PSDB; AAA63941.
XX
PT   Novel polypeptides comprising tumour necrosis factor ligand family
PT   proteins, useful for treating inflammatory and immune disorders, e.g.
PT   rheumatoid arthritis -
XX
PS   Claim 4; Fig 1; 71pp; English.
XX
CC   The present sequence represents a human AGP-3 polypeptide. AGP-3 is a
CC   tumour necrosis factor (TNF) ligand family member. AGP-3 is a type II
CC   transmembrane protein, and is a potent B cell stimulatory factor.
CC   Expression of AGP-3 correlates to increases in the number of B cells
CC   and immunoglobulins produced. AGP-3 proteins, antibodies, and nucleic
CC   acids may be used to treat inflammatory and immune disorders,
CC   e.g. rheumatoid arthritis, Crohn's disease, lupus and graft versus
CC   host disease. The nucleic acids may be used to regulate the expression
CC   of an AGP-3 related protein. The AGP-3 proteins, antibodies and nucleic
CC   ands are also useful for the detection of AGP-3 agonists, antagonists
CC   and characterizing interactions with AGP-3 related proteins.
CC   note: this sequence is not specifically claimed. It is only mentioned
CC   in the claims, in that a polypeptide that does not comprise the present
CC   sequence is claimed.
XX
SQ   Sequence   285 AA;

  Query Match             100.0%;  Score 1451;  DB 21;  Length 285;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-145;
  Matches  285;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60

Qy         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120

Qy        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
```

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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180

Qy        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240

Qy        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
                |||||||||||||||||||||||||||||||||||||||||||||
Db        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285


RESULT 11
AAE09242
ID   AAE09242 standard; Protein; 285 AA.
XX
AC   AAE09242;
XX
DT   19-NOV-2001  (first entry)
XX
DE   Human TALL-1 protein.
XX
KW   Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor;
KW   TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
KW   autoimmune disease; rheumatoid arthritis; multiple sclerosis;
KW   psoriasis.
XX
OS   Homo sapiens.
XX
PN   WO200160397-A1.
XX
PD   23-AUG-2001.
XX
PF   28-NOV-2000; 2000WO-US32378.
XX
PR   16-FEB-2000; 2000US-0182938.
PR   22-AUG-2000; 2000US-0226986.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Dodge KH,  Grewal I,  Kim KJ,  Marsters SA,  Pitti RM;
PI   Yan M;
XX
DR   WPI; 2001-541628/60.
DR   N-PSDB; AAD15903.
XX
PT   Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
PT   activity, for treating autoimmune disorders and cancer, comprises
PT   exposing the cells to TALL-1 or APRIL polypeptide agonists or
PT   antagonists  -
XX
PS   Claim 2; Fig 3; 160pp; English.
XX
CC   The invention relates to methods of using one or more agonists or
CC   antagonists to modulate the activity of the members of TNF (tumour
CC   necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR)
CC   e.g. TACI or BCMA. The method is useful for treating pathological
CC   conditions or diseases associated with increased TALL-1 and APRIL
CC   expression or activity. TALL-1 and APRIL antagonists are used to
CC   block the interaction between APRIL and TALL-1 with TACI or BCMA.
CC   They are useful for treating a mammal suffering from cancer such
CC   as leukaemia, lymphoma, myeloma, cancers of lung and colon and
CC   autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis,
CC   psoriasis and lupus erythematosus. The present sequence is human
CC   TALL-1 protein.
XX
SQ   Sequence   285 AA;

  Query Match           100.0%;  Score 1451;  DB 22;  Length 285;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-145;
  Matches  285;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60

Qy         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120

Qy        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180

Qy        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240

Qy        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
                |||||||||||||||||||||||||||||||||||||||||||||
Db        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285


RESULT 12
AAE07156
ID   AAE07156 standard; Protein; 285 AA.
XX
AC   AAE07156;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human tumour necrosis factor (TNF)-delta protein.
XX
KW   Human; tumour necrosis factor; TNF-delta; gene therapy; antirheumatic;
KW   apoptosis; rheumatoid arthritis; cytostatic; sepsis; anti-inflammatory;
KW   inflammatory bowel disease; immunosuppressive; antiarthritic; tumour;
KW   antibacterial; cancer.
XX
OS   Homo sapiens.
XX
PN   US2001010925-A1.
XX
PD   02-AUG-2001.
XX
PF   17-NOV-1997;   97US-0971317.
XX
PR   17-NOV-1997;   97US-0971317.
XX
PA   (WILE/) WILEY S R.
XX
PI   Wiley SR;
XX
DR   WPI; 2001-496166/54.
DR   N-PSDB; AAD13435.
XX
PT   New tumor necrosis factors (TNF)-delta polynucleotide and polypeptide,
PT   useful in gene therapy, particularly for treating inflammation, and for
PT   inducing apoptosis in cancer and tumor-associated cells to treat cancer
PT    -
XX
PS   Claim 16; Page 36-37; 46pp; English.
XX
CC   The present sequence is human tumor necrosis factor (TNF)-delta protein.
CC   The TNF-delta polynucleotide is useful in gene therapy for modulating
CC   TNF-delta. TNF-delta is useful for treating deficiencies of TNF-delta
CC   and diseases ameliorated by TNF-delta. TNF-delta is also useful for
CC   screening, diagnosing, prognosing, staging or monitoring conditions
CC   or diseases attributable to TNF-delta, e.g. inflammation (e.g.
CC   inflammatory bowel disease, sepsis or rheumatoid arthritis). The
CC   TNF-delta is also useful as an anti-cancer agent to induce apoptosis in
CC   cancer and tumour-associated cells.
XX
SQ   Sequence   285 AA;

  Query Match           100.0%;  Score 1451;  DB 22;  Length 285;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-145;
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```
  Matches  285;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60

Qy         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120

Qy        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180

Qy        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240

Qy        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
              |||||||||||||||||||||||||||||||||||||||||||||
Db        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285


RESULT 13
AAE07879
ID   AAE07879 standard; Protein; 285 AA.
XX
AC   AAE07879;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Human BAFF protein.
XX
KW   Human; tumour necrosis factor; TNF; APBF; APRIL; BAFF; therapy; melanoma;
KW   immune system-related disorder; cancer; renal cell; breast; stomach;
KW   rectal; colon; throat; bladder; ovarian carcinoma; cellular disorder;
KW   gastrointestinal; scleroderma; Kaposi's sarcoma; chronic leukaemia;
KW   squamous cell carcinoma; hyperproliferative condition; pannus formation;
KW   rheumatoid arthritis; postsurgical scarring; fibrosis; liver; uterine;
KW   lung; immunodeficiency; inflammatory disease; lymphadenopathy; vulnerary;
KW   autoimmune disease; graft versus host disease; dermatological;
KW   antiinflammatory; immunosuppressive; cytostatic.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          1..46
FT                   /label= Intracellular_domain
FT   Domain          47..72
FT                   /label= Transmembrane_domain
FT   Domain          73..285
FT                   /label= Extracellular_domain
XX
PN   WO200158949-A2.
XX
PD   16-AUG-2001.
XX
PF   08-FEB-2001; 2001WO-US04121.
XX
PR   11-FEB-2000; 2000US-0181670.
XX
PA   (BIOJ ) BIOGEN INC.
XX
PI   Rennert PD,  Thompson JS,  Ambrose C,  Cachero TG;
XX
DR   WPI; 2001-514644/56.
DR   N-PSDB; AAD14417.
XX
PT   New heteromeric ligand of tumor necrosis factor (TNF) family, useful
PT   for diagnosis, treatment of immune system-related disorders in humans,
PT   comprises TNF-family member APRIL subunit linked non-covalently to
PT   TNF-family member BAFF subunit  -
XX
PS   Claim 2; Fig 2b; 42pp; English.
XX
CC   The present invention relates to an isolated heteromeric ligand of
CC   tumour necrosis factor (TNF)-family, referred to as APBF comprising a
CC   TNF-family member APRIL subunit linked non-covalently to TNF-family
CC   member BAFF subunit. APBF is useful for diagnosis or treatment of
CC   various immune system-related disorders in mammals, preferably humans.
CC   Such disorders include cancer, including cellular disorders, for e.g.
CC   renal cell cancer, Kaposi's sarcoma, chronic leukaemia, breast cancer,
CC   sarcoma, ovarian carcinoma, rectal cancer, throat cancer, melanoma,
CC   colon cancer, bladder cancer, squamous cell carcinoma and
CC   gastrointestinal or stomach cancer, cellular hyperproliferative
CC   conditions, such as scleroderma, pannus formation in rheumatoid
CC   arthritis, postsurgical scarring and lung, liver and uterine fibrosis
CC   and immunodeficiencies, inflammatory diseases, lymphadenopathy,
CC   autoimmune diseases and graft versus host disease. APBF is also useful
CC   for producing monoclonal or polyclonal antibodies and for identifying
CC   novel modulators affecting biological function and receptors interacting
CC   with APBF. The present sequence is human BAFF protein.
XX
SQ   Sequence   285 AA;

  Query Match             100.0%;  Score 1451;  DB 22;  Length 285;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-145;
  Matches  285;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60

Qy         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120

Qy        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180

Qy        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240

Qy        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
              |||||||||||||||||||||||||||||||||||||||||||||
Db        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285


RESULT 14
AAU12183
ID   AAU12183 standard; Protein; 285 AA.
XX
AC   AAU12183;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human PRO738 polypeptide sequence.
XX
KW   Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW   breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW   cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
KW   adipocyte; A-peptide; factor VIIA; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200140466-A2.
XX
PD   07-JUN-2001.
XX
PF   01-DEC-2000; 2000WO-US32678.
XX
PR   01-DEC-1999;   99WO-US28301.
PR   01-DEC-1999;   99WO-US28634.
PR   02-DEC-1999;   99WO-US28551.
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PR   02-DEC-1999;   99WO-US28564.
PR   02-DEC-1999;   99WO-US28565.
PR   09-DEC-1999;   99US-0170262.
PR   16-DEC-1999;   99WO-US30095.
PR   20-DEC-1999;   99WO-US30911.
PR   20-DEC-1999;   99WO-US30999.
PR   30-DEC-1999;   99WO-US31243.
PR   06-JAN-2000; 2000WO-US00277.
PR   06-JAN-2000; 2000WO-US00376.
PR   11-FEB-2000; 2000WO-US03565.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   22-FEB-2000; 2000WO-US04414.
PR   24-FEB-2000; 2000WO-US04914.
PR   24-FEB-2000; 2000WO-US05004.
PR   01-MAR-2000; 2000WO-US05601.
PR   20-MAR-2000; 2000WO-US07377.
PR   21-MAR-2000; 2000WO-US07532.
PR   30-MAR-2000; 2000WO-US08439.
PR   17-MAY-2000; 2000WO-US13705.
PR   22-MAY-2000; 2000WO-US14042.
PR   30-MAY-2000; 2000WO-US14941.
PR   02-JUN-2000; 2000WO-US15264.
PR   10-NOV-2000; 2000WO-US30873.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Beresini M,  Deforge L,  Desnoyers L,  Filvaroff E,  Gao W;
PI   Gerritsen ME,  Goddard A,  Godowski PJ,  Gurney AL,  Sherwood S;
PI   Smith V,  Stewart TA,  Tumas D,  Watanabe CK,  Wood WI,  Zhang Z;
XX
DR   WPI; 2001-408281/43.
DR   N-PSDB; AAS21255.
XX
PT   Isolated, secretory and transmembrane PRO polypeptide used to detect
PT   other PRO polypeptides, link bioactive molecules to cells expressing
PT   PRO polypeptides, and detect the presence of mammalian tumours e.g.
PT   lung, breast, prostate, cervical -
XX
PS   Claim 12; Fig 24; 813pp; English.
XX
CC   AAU12172-AAU12446 represent novel human secretory and transmembrane
CC   PRO polypeptides. The PRO polypeptides are useful to detect other
CC   PRO polypeptides, to link bioactive molecules to cells expressing
CC   PRO polypeptides, to modulate biological activities of cells expressing
CC   PRO polypeptides, and to detect the presence of mammalian lung, colon,
CC   breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC   polypeptide expression in a cell sample to that in a control sample.
CC   Some of the 275 sequences are also useful to stimulate the release of
CC   tumour necrosis factor-alpha (TNF-alpha) from human blood, the
CC   proliferation or differentiation of chondrocytes, the proliferation or
CC   gene expression in pericyte cells, the release of proteoglycans from
CC   cartilage, the proliferation of inner ear utricular supporting cells or
CC   of T-lymphocytes, the release of a cytokine from peripheral blood
CC   monocytes (PBMCs), or the proliferation of endothelial cells. Some of
CC   the PRO polypeptides may modulate glucose or free fatty acid uptake by
CC   skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
CC   to factor VIIA. The PRO polypeptides can be used in assays to identify
CC   molecules involved in binding interactions. The polynucleotides encoding
CC   PRO polypeptides can be used to generate probes, antisense RNA/DNA,
CC   transgenic or knock out animals and can be used in gene therapy.
XX
SQ   Sequence   285 AA;

  Query Match           100.0%;  Score 1451;  DB 22;  Length 285;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-145;
  Matches  285;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60

Qy         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120

Qy        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180

Qy        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240

Qy        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
              |||||||||||||||||||||||||||||||||||||||||||||
Db        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285


RESULT 15
AAY71915
ID   AAY71915 standard; Protein; 285 AA.
XX
AC   AAY71915;
XX
DT   26-MAR-2001  (first entry)
XX
DE   Human TACI-ligand (TACI-L) protein.
XX
KW   Human; transmembrane activator and CAML interactor; TACI;
KW   tumour necrosis factor receptor; TNF; autoimmune disease; diabetes;
KW   calcium-signal modulating cyclophilin ligand; CAML; viral infection;
KW   neutrokine alpha polypeptide; TACI-Ligand; TACI-L; cytostatic; therapy;
KW   neuroprotective; antidiabetic; antiviral; antiinflammatory; tumour;
KW   antiarthritic; antirheumatic; immunosuppressive; multiple sclerosis;
KW   rheumatoid arthritis; graft rejection; inflammation; cell proliferation;
KW   cell death; immunoglobulin E-mediated allergic reaction; IgE.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          1..46
FT                   /label= Intracellular_domain
FT   Domain          47..72
FT                   /label= Transmembrane_domain
FT   Domain          73..285
FT                   /label= Extracellular_domain
FT   Binding-site    123..285
FT                   /label= TACI_binding_site
FT                   /note= "Binds with extracellular domain of TACI"
XX
PN   WO200067034-A1.
XX
PD   09-NOV-2000.
XX
PF   14-APR-2000; 2000WO-US10282.
XX
PR   30-APR-1999;   99US-0302863.
XX
PA   (IMMU ) IMMUNEX CORP.
XX
PI   Goodwin RG,  Din WS;
XX
DR   WPI; 2001-016005/02.
DR   N-PSDB; AAD02007.
XX
PT   Use of new interactions between tumour necrosis factor receptors (TACI)
PT   and TACI ligands to screen candidate molecules for determining agonist
PT   and antagonist interactions which are used for treating inflammation -
XX
PS   Claim 10; Fig 2b; 46pp; English.
XX
CC   The present sequence is a human tumour necrosis factor receptor
CC   (TACI)-ligand (TACI-L) protein.
CC   TACI (Transmembrane activator and calcium-signal modulating
CC   cyclophilin ligand (CAML)-interactor) forms a complex with neutrokine
```

CC alpha polypeptide (TACI-Ligand). The antagonist or agonist of
CC TACI/TACI-L complex is useful for modulating an intracellular signalling
CC cascade mediated by TACI/TACI-L complex. Antagonists of TACI/TACI-L
CC complex are used to inhibit the interaction between TACI and TACI-L for
CC therapeutic purposes to treat tumour and tumour metastasis and to combat
CC various autoimmune diseases e.g. multiple sclerosis and diabetes, as
CC well as other disorders, such as viral infection, rheumatoid arthritis,
CC graft rejection, and immunoglobulin (Ig) E-mediated allergic reactions
CC and inflammation. The interaction is used to study cellular processes
CC associated with tumour necrosis factor (TNF)-receptors such as immune
CC regulation, cell proliferation, cell death and inflammatory responses.
CC The interaction between the extracellular region of TACI and TACI-L can
CC be used to further develop understanding of which cell types TACI-L
CC acts upon.
XX
SQ Sequence 285 AA;

Query Match 100.0%; Score 1451; DB 22; Length 285;
Best Local Similarity 100.0%; Pred. No. 4.4e-145;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60

Qy         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120

Qy        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180

Qy        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240

Qy        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
              |||||||||||||||||||||||||||||||||||||||||||||
Db        241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
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Search completed: August 28, 2003, 18:03:25
Job time : 88 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 28, 2003, 18:00:51 ; Search time 40 Seconds
(without alignments)
685.202 Million cell updates/sec

Title: US-09-507-968D-2
Perfect score: 1451
Sequence: 1 MDDSTEREQSRLTSCLKKRE.....ENAQISLDGDVTFFGALKLL 285

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	110.5	7.6	235	2	JU0029	tumor necrosis fac
2	109.5	7.5	233	2	S11688	tumor necrosis fac
3	109.5	7.5	235	1	QWMSN	tumor necrosis fac
4	108	7.4	233	1	S24642	tumor necrosis fac
5	107.5	7.4	235	2	I54490	tumor necrosis fac
6	107	7.4	193	2	S06192	tumor necrosis fac
7	107	7.4	232	1	S12606	tumor necrosis fac
8	102.5	7.1	234	1	JH0529	tumor necrosis fac
9	100.5	6.9	205	1	QWHUX	lymphotoxin alpha
10	98.5	6.8	233	1	QWHUN	tumor necrosis fac
11	98	6.8	234	1	A25451	tumor necrosis fac
12	97.5	6.7	184	2	A82993	hypothetical prote
13	97.5	6.7	281	2	I38707	Fas ligand - human
14	94.5	6.5	347	2	A75537	hypothetical prote
15	93.5	6.4	651	1	RGBYD2	translation regula
16	93	6.4	596	2	B96834	hypothetical prote
17	92.5	6.4	185	2	S52715	tumor necrosis fac
18	90.5	6.2	204	1	S17289	tumor necrosis fac
19	89.5	6.2	233	1	S22052	tumor necrosis fac
20	89.5	6.2	234	1	JQ1344	tumor necrosis fac
21	88.5	6.1	631	2	AE3565	hypothetical prote
22	87.5	6.0	919	2	F83257	hypothetical prote
23	87.5	6.0	993	2	A38437	probable homeotic
24	87	6.0	273	2	T49495	probable phosphoma
25	86.5	6.0	1229	2	D85023	P-glycoprotein-lik
26	86.5	6.0	1229	2	T52319	P-glycoprotein-lik
27	85.5	5.9	204	1	S24641	lymphotoxin - bovi
28	85.5	5.9	351	2	S40840	hypothetical 39.3K
29	85.5	5.9	358	1	W2WL51	E2 protein - human
30	84.5	5.8	557	2	B83962	hypothetical prote
31	84.5	5.8	595	2	E87698	sensor histidine k
32	84	5.8	197	1	JH0309	tumor necrosis fac
33	84	5.8	295	2	B41320	hypothetical prote
34	84	5.8	461	2	T23574	hypothetical prote
35	84	5.8	493	2	C87362	hypothetical prote
36	83.5	5.8	351	2	F91231	hypothetical prote
37	83.5	5.8	351	2	E86078	hypothetical prote
38	83.5	5.8	462	2	T50422	homolog to yeast o
39	83	5.7	426	2	T21001	hypothetical prote
40	83	5.7	957	2	AH2227	cation-transportin
41	82.5	5.7	371	1	A43830	alanine dehydrogen
42	82.5	5.7	478	1	I47154	transcription fact
43	82.5	5.7	574	2	S04333	lamin C - mouse
44	82.5	5.7	665	2	S28182	lamin A - mouse
45	82.5	5.7	680	2	A43800	nuclear autoantige

ALIGNMENTS

RESULT 1
JU0029
tumor necrosis factor alpha precursor - rat
N;Alternate names: cachectin; TNF alpha
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 04-Feb-2000
C;Accession: JU0029; JN0868; S21674
R;Shirai, T.; Shimizu, N.; Horiguchi, S.; Ito, H.
Agric. Biol. Chem. 53, 1733-1736, 1989
A;Title: Cloning and expression in Escherichia coli of the gene for rat tumor necrosi
A;Reference number: JU0029
A;Accession: JU0029
A;Molecule type: DNA
A;Residues: 1-235 <SHI>
R;Kwon, J.; Chung, I.Y.; Benveniste, E.N.
Gene 132, 227-236, 1993
A;Title: Cloning and sequence analysis of the rat tumor necrosis factor-encoding gene
A;Reference number: JN0868; MUID:94040766; PMID:8224868
A;Accession: JN0868
A;Molecule type: DNA
A;Residues: 1-235 <KWO>
A;Cross-references: GB:L00981; NID:g205253; PIDN:AAA16275.1; PID:g205254
R;Estler, H.C.; Grewe, M.; Gaussling, R.; Pavlovic, M.; Decker, K.
Biol. Chem. Hoppe-Seyler 373, 271-281, 1992
A;Title: Rat tumor necrosis factor-alpha. Transcription in rat Kupffer cells and in v
A;Reference number: S21674; MUID:92329007; PMID:1627266
A;Accession: S21674
A;Molecule type: mRNA
A;Residues: 1-38,'P',40-162,'T',164-201,'S',203-235 <EST>
A;Cross-references: GB:X66539; GB:S40199; NID:g395369; PIDN:CAA47146.1; PID:g395370
C;Comment: Tumor necrosis factor is secreted by macrophages in response to endotoxin
C;Genetics:
A;Gene: TNF-alpha
A;Introns: 62/3; 81/1; 97/1
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; m
F;80-235/Product: tumor necrosis factor #status predicted <MAT>
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;86/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;148-179/Disulfide bonds: #status predicted

Query Match 7.6%; Score 110.5; DB 2; Length 235;
Best Local Similarity 22.2%; Pred. No. 0.057;
Matches 54; Conservative 45; Mismatches 87; Indels 57; Gaps 11;

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Qy         60 CLTVVSFYQVAALQGDLASLRAELQG-HHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPP 118
              ||:: ||  ||        |   : | :  || | |       |  : | |  |:
Db         32 CLSLFSFLLVAGATTLFCLLNFGVIGPNKEEKFPNG-----LPLISSMAQTLTLR----- 81

Qy        119 APGEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSAL 178
                    :||||| :|          :: |: ::      :  |               :
```

```
Db         82 -----SSSQNSSDKPVAHVVANHQAEEQLEWLSQRANALLANG----------------M 120

Qy        179 EEKENKILVKETGYFFIYGQVLYTDK----TYAMGHLIQRKKVHVFGDELSLVTLFR--C 232
              : |:|:::|   | : || |||:  :       : | : |  :  : :::||::  :  |
Db        121 DLKDNQLVVPADGLYLIYSQVLFKGQGCPDYVLLTHTVSRFAIS-YQEKVSLLSAIKSPC 179

Qy        233 IQNMPETLP----NNSCYSAGIAKLEEGDELQLAIPRENAQISLDG--DVT-----FFGA 281
               :: ||          |  |: :||:|| |       :|:::|    |:|     :||
Db        180 PKDTPEGAELKPWYEPMYLGGVFQLEKGDLL-------SAEVNLPKYLDITESGQVYFGV 232

Qy        282 LKL 284
              : |
Db        233 IAL 235


RESULT 2
S11688
tumor necrosis factor alpha precursor - cat
C;Species: Felis silvestris catus (domestic cat)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 04-Feb-2000
C;Accession: S11688
R;McGraw, R.A.; Coffee, B.W.; Otto, C.M.; Drews, R.T.; Rawlings, C.A.
Nucleic Acids Res. 18, 5563, 1990
A;Title: Gene sequence of feline tumor necrosis factor alpha.
A;Reference number: S11688; MUID:91016860; PMID:2216740
A;Accession: S11688
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-233 <MCG>
A;Cross-references: EMBL:X54000; NID:g1084; PIDN:CAA37948.1; PID:g295777
C;Genetics:
A;Introns: 62/3; 78/1; 94/1
C;Superfamily: tumor necrosis factor
C;Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;145-177/Disulfide bonds: #status predicted

  Query Match             7.5%;  Score 109.5;  DB 2;  Length 233;
  Best Local Similarity   22.7%;  Pred. No. 0.068;
  Matches   55;  Conservative   35;  Mismatches   95;  Indels   57;  Gaps   10;

Qy         60 CLTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPA 119
              ||:: ||  ||        |   : |   |:||                  ||::  |
Db         32 CLSLFSFLLVAGATTLFCLLHFGVIGPQREELP----------------HGLQLINPLP 74

Qy        120 PGEGNSSQNSRNK---RAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGS 176
                :||:   :|     |  ||    :  || ::      :  |
Db         75 QTLRSSSRTPSDKPVAHVVANPE---AEGQLQRLSRRANALLANG-------------- 116

Qy        177 ALEEKENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFG----DELSLVTLFR- 231
               :|  :|:: |   | : || |||:| :     |::    :  |      :::|::  :
Db        117 -VELTDNQLKVPSDGLYLIYSQVLFTGQGCPSTHVLLTHAISRFAVSYQTKVNLLSAIKS 175

Qy        232 -CIQNMPETLPNNSCYS----AGIAKLEEGDELQLAIPRENAQISLD----GDVTFFGAL 282
               | :  ||       |      |: :||:|| |   |   |    ||    | | :|| :
Db        176 PCQRETPEGAEAKPWYEPIYLGGVFQLEKGDRLSTEI---NLPAYLDFAESGQV-YFGII 231

Qy        283 KL 284
              |
Db        232 AL 233


RESULT 3
QWMSN
tumor necrosis factor alpha precursor - mouse
N;Alternate names: cachectin; TNF alpha
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 04-Feb-2000
C;Accession: A22908; S03791; A27303; A25164; A23127; A34251; I59058; A36696
R;Shirai, T.; Shimizu, N.; Shiojiri, S.; Horiguchi, S.; Ito, H.
DNA 7, 193-201, 1988
A;Title: Cloning and expression in Escherichia coli of the gene for mouse tumor necrosis
A;Reference number: A22908; MUID:88224564; PMID:2836146
A;Accession: A22908
A;Molecule type: DNA
A;Residues: 1-235 <SHI>
A;Cross-references: GB:M20155
R;Shakhov, A.N.; Nedospasov, S.A.
Bioorg. Khim. 13, 701-705, 1987
A;Title: Molecular cloning of the genes coding for tumor necrosis factors: complete n
A;Reference number: S03791; MUID:87298639; PMID:3040015
A;Accession: S03791
A;Molecule type: DNA
A;Residues: 1-235 <SHA>
A;Cross-references: GB:M38296; NID:g202086; PIDN:AAA40459.1; PID:g202087
A;Note: article in Russian with English abstract
R;Semon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A.
Nucleic Acids Res. 15, 9083-9084, 1987
A;Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha-(tumor
A;Reference number: A93679; MUID:88067722; PMID:3684584
A;Accession: A27303
A;Molecule type: DNA
A;Residues: 1-235 <SEM>
A;Cross-references: GB:Y00467; NID:g54830; PIDN:CAA68530.1; PID:g54832
R;Pennica, D.; Hayflick, J.S.; Bringman, T.S.; Palladino, M.A.; Goeddel, D.V.
Proc. Natl. Acad. Sci. U.S.A. 82, 6060-6064, 1985
A;Title: Cloning and expression in Escherichia coli of the cDNA for murine tumor necr
A;Reference number: A25164; MUID:85298296; PMID:3898078
A;Accession: A25164
A;Molecule type: mRNA
A;Residues: 1-235 <PEN>
A;Cross-references: GB:M11731; NID:g202084; PIDN:AAA40458.1; PID:g202085
R;Fransen, L.; Muller, R.; Marmenout, A.; Tavernier, J.; van der Heyden, J.; Kawashim
Nucleic Acids Res. 13, 4417-4429, 1985
A;Title: Molecular cloning of mouse tumour necrosis factor cDNA and its eukaryotic ex
A;Reference number: A23127; MUID:85242112; PMID:2989794
A;Accession: A23127
A;Molecule type: mRNA
A;Residues: 1-235 <FRA>
A;Cross-references: GB:X02611; NID:g54844; PIDN:CAA26457.1; PID:g54845
R;Cseh, K.; Beutler, B.
J. Biol. Chem. 264, 16256-16260, 1989
A;Title: Alternative cleavage of the cachectin/tumor necrosis factor propeptide resul
A;Reference number: A34251; MUID:89380231; PMID:2777790
A;Accession: A34251
A;Molecule type: protein
A;Residues: 70-87 <CSE>
R;Caput, D.; Beutler, B.; Hartog, K.; Thayer, R.; Brown-Shimer, S.L.; Cerami, A.
Proc. Natl. Acad. Sci. U.S.A. 83, 1670-1674, 1986
A;Title: Identification of a common nucleotide sequence in the 3'-untranslated region
A;Reference number: I59058; MUID:86149365; PMID:2419912
A;Accession: I59058
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-230,'R',232-235 <RES>
A;Cross-references: GB:M13049; NID:g202082; PIDN:AAA40457.1; PID:g202083
R;Sherry, B.; Jue, D.M.; Zentella, A.; Cerami, A.
Biochem. Biophys. Res. Commun. 173, 1072-1078, 1990
A;Title: Characterization of high molecular weight glycosylated forms of murine tumor
A;Reference number: A36696; MUID:91097531; PMID:2268312
A;Accession: A36696
A;Molecule type: protein
A;Residues: 80-85,'X',87-99 <SHE>
C;Genetics:
A;Introns: 62/3; 81/1; 97/1
A;Note: the first intron occurs in the 5'-untranslated region
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; m
F;80-235/Product: tumor necrosis factor #status experimental <MAT>
F;20/Binding site: myristate (Lys) (covalent) #status predicted
F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;86/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;148-179/Disulfide bonds: #status predicted

  Query Match             7.5%;  Score 109.5;  DB 1;  Length 235;
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  Best Local Similarity   21.0%;  Pred. No. 0.069;
  Matches   51;  Conservative   48;  Mismatches   87;  Indels   57;  Gaps   11;

Qy         60 CLTVVSFYQVAALQGDLASLRAELQG-HHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPP 118
              ||:: ||  ||        |   : |    || | |       |  : | |  |:
Db         32 CLSLFSFLLVAGATTLFCLLNFGVIGPQRDEKFPNG-----LPLISSMAQTLTLR----- 81

Qy        119 APGEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSAL 178
                   :|||||  :|           :: |: ::      :  |                :
Db         82 -----SSSQNSSDKPVAHVVANHQVEEQLEWLSQRANALLANG----------------M 120

Qy        179 EEKENKILVKETGYFFIYGQVLYTDK----TYAMGHLIQRKKVHVFGDELSLVTLFR--C 232
              : |:|:::|   | : :| |||:  :       : | : |  :  : ::::|::  :  |
Db        121 DLKDNQLVVPADGLYLVYSQVLFKGQGCPDYVLLTHTVSRFAIS-YQEKVNLLSAVKSPC 179

Qy        233 IQNMPETLP----NNSCYSAGIAKLEEGDEL--QLAIPR-----ENAQISLDGDVTFFGA 281
               :: ||         |  |: :||:||:|  :: :|:     |: |:       :||
Db        180 PKDTPEGAELKPWYEPIYLGGVFQLEKGDQLSAEVNLPKYLDFAESGQV-------YFGV 232

Qy        282 LKL 284
              : |
Db        233 IAL 235


RESULT 4
S24642
tumor necrosis factor alpha precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C;Accession: I46047; S24642
R;Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.
Cytokine 5, 336-341, 1993
A;Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and tu
A;Reference number: I46046; MUID:94083525; PMID:8260599
A;Accession: I46047
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-233 <CL2>
A;Cross-references: EMBL:Z14137; NID:g796; PIDN:CAA78511.1; PID:g798
C;Genetics:
A;Gene: TNFA
A;Introns: 62/3; 78/1; 94/1
C;Superfamily: tumor necrosis factor
C;Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
F;20/Binding site: myristate (Lys) (covalent) #status predicted
F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;145-177/Disulfide bonds: #status predicted

  Query Match             7.4%;  Score 108;  DB 1;  Length 233;
  Best Local Similarity   22.8%;  Pred. No. 0.092;
  Matches   56;  Conservative   42;  Mismatches   88;  Indels   60;  Gaps   12;

Qy         58 SC-CLTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFE 116
              || ||:: ||  ||        |   : |   |: | |           |:: :
Db         29 SCLCLSLFSFLLVAGATTLFCLLHFGVIGPQREESPGG----------PSINS------ 71

Qy        117 PPAPGEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGS 176
              |      :||| | ||               ::||  :|   :   ::   |::   |
Db         72 PLVQTLRSSSQASSNKPVA-----------HVVADINSPGQLRWWDSYANALMA--NGV 117

Qy        177 ALEEKENKILVKETGYFFIYGQVLYTDK-----TYAMGHLIQRKKVHVFGDELSLVTLFR 231
               ||  :|:::|   | : || |||:  :       : | | |  |  :  ::::::  :
Db        118 KLE--DNQLVVPADGLYLIYSQVLFRGQGCPSTPLFLTHTISRIAVS-YQTKVNILSAIK 174

Qy        232 --CIQNMPETLP----NNSCYSAGIAKLEEGDELQLAIPRENAQISL-------DGDVTF 278
                | :  ||          |  |: :||:|| |       :|:|:|       :    :
Db        175 SPCHRETPEWAEAKPWYEPIYQGGVFQLEKGDRL-------SAEINLPDYLDYAESGQVY 227

Qy        279 FGALKL 284
              || : |
Db        228 FGIIAL 233


RESULT 5
I54490
tumor necrosis factor alpha precursor - white-footed mouse
C;Species: Peromyscus leucopus (white-footed mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 04-Feb-2000
C;Accession: I54490
R;Crew, M.D.; Filipowsky, M.E.
Immunogenetics 35, 351-353, 1992
A;Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus l
A;Reference number: I54490; MUID:92218012; PMID:1348497
A;Accession: I54490
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-235 <RES>
A;Cross-references: GB:M59233; NID:g202506; PIDN:AAA40596.1; PID:g202507
C;Genetics:
A;Gene: PlTNF
A;Introns: 62/3; 81/1; 97/1
C;Superfamily: tumor necrosis factor
C;Keywords: glycoprotein; lipoprotein; myristylation
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted

  Query Match             7.4%;  Score 107.5;  DB 2;  Length 235;
  Best Local Similarity   22.0%;  Pred. No. 0.1;
  Matches   54;  Conservative   46;  Mismatches   84;  Indels   61;  Gaps   14;

Qy         60 CLTVVSFYQVAALQGDLASLRAELQG-HHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPP 118
              ||:: ||  ||        |   : |    || |      |  |   : | |  |:
Db         32 CLSLFSFLLVAGATTLFCLLNFGVIGPQREEKFP--NNLPIIG---SMAQTLTLR----- 81

Qy        119 APGEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSAL 178
                   :|||||  :|          |          | :   : :|:   :          : :
Db         82 -----SSSQNSSDK--------PVAHVVANHQVDEQLEWLSRGANALL--------ANGM 120

Qy        179 EEKENKILVKETGYFFIYGQVLYTDK---TYA-MGHLIQRKKVHVFGDELSLVTLFRCIQ 234
              : |:|::::   | : :| |||:  :   :|  : | : |  |  : |:::|::  :
Db        121 DLKDNQLVIPADGLYLVYSQVLFKGQGCSSYVLLTHTVSRFAVS-YEDKVNLLSAIK--S 177

Qy        235 NMPETLPNNS--------CYSAGIAKLEEGDEL--QLAIPR-----ENAQISLDGDVTFF 279
                |:  |  |          |  |: :||:|| |  :: :|:     |: |:      :|
Db        178 PCPKETPEGSELKPWYEPIYLGGVFQLEKGDRLSAEVNLPKYLDFAESGQV-------YF 230

Qy        280 GALKL 284
              | : |
Db        231 GVIAL 235


RESULT 6
S06192
tumor necrosis factor alpha precursor - goat (fragment)
N;Alternate names: cachectin; TNF alpha
C;Species: Capra aegagrus hircus (domestic goat)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 31-Jan-2000
C;Accession: S06192; S41867
R;Goldstein, I.M.; Henner, D.; Talhouk, A.
submitted to the EMBL Data Library, March 1989
A;Reference number: S06192
A;Accession: S06192
A;Molecule type: mRNA
A;Residues: 1-193 <GOL>
A;Cross-references: EMBL:X14828; NID:g992; PIDN:CAA32937.1; PID:g993
R;Rimstad, E.
submitted to the EMBL Data Library, January 1994
A;Reference number: S41867
A;Accession: S41867
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 36-38,'S',40-78,'A',80-88,'N',90-114,'Q',116-123,'D',125-144,'G',145-173,
A;Cross-references: EMBL:X77317; NID:g452607; PIDN:CAA54523.1; PID:g452608
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage; membrane prote
F;42/Binding site: carbohydrate (Ser) (covalent) #status predicted
```

```
F;106-138/Disulfide bonds: #status predicted

  Query Match             7.4%;  Score 107;  DB 2;  Length 193;
  Best Local Similarity   23.4%;  Pred. No. 0.089;
  Matches   50;  Conservative   36;  Mismatches   92;  Indels   36;  Gaps   10;

Qy         84 QGHHAEKLPA---GAGAPKAGLEEAPAVTAGLKIFEPPAPGEGNSSQNSRNKRAVQGPEE 140
              : |||  |||   |   |:   |::|   ||     |      :||| | ||
Db          3 RSHHA-LLPAALRGNRPPEE--EQSP---AGPSFNRPLVQTLRSSSQASSNKPVA----- 51

Qy        141 TVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEEKENKILVKETGYFFIYGQVL 200
                  ::|:   |    |   :    :  : : :| |:|:::|   | : || |||
Db         52 -------HVVANISAP----GQLRWGDSYANALKANGVELKDNQLVVPTDGLYLIYSQVL 100

Qy        201 Y-----TDKTYAMGHLIQRKKVHVFGDELSLVTLFR--CIQNMPETLPN---NSCYSAGI 250
              :          : | | |   |  :  ::::::  :  | :  ||          |  |:
Db        101 FRGHGCPSTPLFLTHTISRIAVS-YQTKVNILSAIKSPCHRETPEAEAKPWYEPIYQGGV 159

Qy        251 AKLEEGDELQLAIPRENAQISLDGDVTFFGALKL 284
               :||:|| |   | :       :    :|| : |
Db        160 FQLEKGDRLSAEINQPEYLDYAESGQVYFGIIAL 193


RESULT 7
S12606
tumor necrosis factor alpha precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C;Accession: S12606; S17290; S18965; I46659
R;Drews, R.T.; Coffee, B.W.; Prestwood, A.K.; McGraw, R.A.
Nucleic Acids Res. 18, 5564, 1990
A;Title: Gene sequence of porcine tumor necrosis factor alpha.
A;Reference number: S12606; MUID:91016861; PMID:2216741
A;Accession: S12606
A;Molecule type: DNA
A;Residues: 1-232 <DRE>
A;Cross-references: EMBL:X54001; NID:g2135; PIDN:CAA37949.1; PID:g2136
R;Kuhnert, P.; Wuethrich, C.; Peterhans, E.; Pauli, U.
Gene 102, 171-178, 1991
A;Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative anal
A;Reference number: S17289; MUID:91340150; PMID:1874444
A;Accession: S17290
A;Molecule type: DNA
A;Residues: 1-232 <KUH>
A;Cross-references: EMBL:X54859; NID:g2132; PIDN:CAA38639.1; PID:g2134
A;Note: the authors translated the codon GAG for residue 202 as Gly
R;Choi, C.S.; Molitor, T.W.; Lin, G.F.; Murtaugh, M.P.
submitted to the EMBL Data Library, January 1991
A;Description: Complete nucleotide sequence of a cDNA encoding porcine tumor necrosis fa
A;Reference number: S18965
A;Accession: S18965
A;Molecule type: mRNA
A;Residues: 1-232 <CHO>
A;Cross-references: EMBL:X57321; NID:g2137; PIDN:CAA40591.1; PID:g2138
R;Pauli, U.; Beutler, B.; Peterhans, E.
Gene 81, 185-191, 1989
A;Title: Porcine tumor necrosis factor alpha: Cloning with the polymerase chain reaction
A;Reference number: I46659; MUID:90034181; PMID:2478420
A;Accession: I46659
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 44-232 <PAU>
A;Cross-references: GB:M29079; NID:g164694; PIDN:AAA31128.1; PID:g164695
C;Genetics:
A;Introns: 62/3; 78/1; 93/1
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; myri
F;1-77/Domain: propeptide #status predicted <PRO>
F;78-232/Product: tumor necrosis factor alpha #status predicted <MAT>
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;144-176/Disulfide bonds: #status predicted

  Query Match             7.4%;  Score 107;  DB 1;  Length 232;
  Best Local Similarity   22.0%;  Pred. No. 0.11;
  Matches   54;  Conservative   40;  Mismatches   86;  Indels   66;  Gaps   11;

Qy         60 CLTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPA 119
              ||:: ||  ||        |  |: |   |: |||                 | |  | |
Db         32 CLSLFSFLLVAGATTLFCLLHFEVIGPQKEEFPAGP---------------LSI-NPLA 74

Qy        120 PGEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKR---GS 176
               |  :||| |          :: |      : |: :           : |   :      :
Db         75 QGLRSSSQTS---------DKPVAHVVANVKAEGQ-----------LQWQSGYANALLAN 114

Qy        177 ALEEKENKILVKETGYFFIYGQVLYTDK-----TYAMGHLIQRKKVHVFGDELSLVTLFR 231
               :: |:|:::|   | : || |||:  :        : | | |  |  :  :::|::  :
Db        115 GVKLKDNQLVVPTDGLYLIYSQVLFRGQGCPSTNVFLTHTISRIAVS-YQTKVNLLSAIK 173

Qy        232 --CIQNMPETLPNNSCYS----AGIAKLEEGDELQLAIPRENAQISL-------DGDVTF 278
                | :  ||       |      |: :||: | |       :|:|:|       :    :
Db        174 SPCQRETPEGAEAKPWYEPIYLGGVFQLEKDDRL-------SAEINLPDYLDFAESGQVY 226

Qy        279 FGALKL 284
               || : |
Db        227 FGIIAL 232


RESULT 8
JH0529
tumor necrosis factor alpha precursor - sheep
N;Alternate names: cachectin; TNF alpha
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C;Accession: JH0529; S48118; S13114; S20661
R;Green, I.R.; Sargan, D.R.
Gene 109, 203-210, 1991
A;Title: Sequence of the cDNA encoding ovine tumor necrosis factor-alpha: problems wi
A;Reference number: JH0529; MUID:92112044; PMID:1765267
A;Accession: JH0529
A;Molecule type: mRNA
A;Residues: 1-234 <GRE>
A;Cross-references: EMBL:X55152; NID:g1405; PIDN:CAA38952.1; PID:g1406
A;Experimental source: alveolar macrophage
R;Nash, A.D.; Barcham, G.J.; Brandon, M.R.; Andrews, A.E.
Immunol. Cell Biol. 69, 273-283, 1991
A;Title: Molecular cloning, expression and characterization of ovine TNF-alpha.
A;Reference number: S48118; MUID:92155784; PMID:1786996
A;Accession: S48118
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-234 <NAS>
A;Cross-references: EMBL:X56756; NID:g297806; PIDN:CAA40076.1; PID:g297807
R;Young, A.J.; Hay, J.B.; Chan, J.Y.C.
Nucleic Acids Res. 18, 6723, 1990
A;Title: Primary structure of ovine tumor necrosis factor alpha cDNA.
A;Reference number: S13114; MUID:91067496; PMID:2251151
A;Accession: S13114
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-62,64-234 <YOU>
A;Cross-references: EMBL:X55966; NID:g1403; PIDN:CAA39437.1; PID:g1404
A;Note: comparison with the introns of homologous sequences suggest that this is prob
C;Superfamily: tumor necrosis factor
C;Keywords: alternative splicing; cytokine; cytotoxin; glycoprotein; lipoprotein; lym
F;1-77/Domain: propeptide #status predicted <PRO>
F;78-234/Product: tumor necrosis factor alpha #status predicted <TUM>
F;20/Binding site: myristate (Lys) (covalent) #status predicted
F;82/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;96/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;146-178/Disulfide bonds: #status predicted

  Query Match             7.1%;  Score 102.5;  DB 1;  Length 234;
  Best Local Similarity   22.5%;  Pred. No. 0.27;
  Matches   56;  Conservative   41;  Mismatches   87;  Indels   65;  Gaps   12;
```

```
Qy         58 SC-CLTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFE 116
              || ||:: ||  ||        |   : |   |             |::|   ||
Db         29 SCWCLSLFSFLLVAGATTLFCLLHFGVIGPQRE------------EQSP---AGPSFNR 72

Qy        117 PPAPGEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGS 176
              |      :||| | ||                 ::|:   |   :   ::   |::    :
Db         73 PLVQTLRSSSQASNNKPVA-----------HVVANISAPGQLRWGDSYANALMA----N 116

Qy        177 ALEEKENKILVKETGYFFIYGQVLY-----TDKTYAMGHLIQRKKVHVFGDELSLVTLFR 231
               :| |:|:::|   | : || |||:          : | | |   |  :  :::::  :
Db        117 GVELKDNQLVVPTDGLYLIYSQVLFRGHGCPSTPLFLTHTISRIAVS-YQTKVNILSAIK 175

Qy        232 --CIQNMPETLPN-------NSCYSAGIAKLEEGDELQLAIPRENAQISL-------DGD 275
                | :   |||           |  |: :||:|| |       :|:|:|       :
Db        176 SPCHR---ETLEGAEAKPWYEPIYQGGVFQLEKGDRL-------SAEINLPEYLDYAESG 225

Qy        276 VTFFGALKL 284
               :|| : |
Db        226 QVYFGIIAL 234
```

RESULT 9
QWHUX
lymphotoxin alpha precursor - human
N;Alternate names: lymphotoxin A; TNF beta; tumor necrosis factor beta (TNF beta)
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence_revision 07-Jul-1995 #text_change 16-Jun-2000
C;Accession: A92755; S36154; I54482; A93350; B32877; A91906; A61478; S26951; A01645; A23
R;Nedwin, G.E.; Jarrett-Nedwin, J.; Smith, D.H.; Naylor, S.L.; Sakaguchi, A.Y.; Goeddel,
J. Cell. Biochem. 29, 171-181, 1985
A;Title: Structure and chromosomal localization of the human lymphotoxin gene.
A;Reference number: A92755; MUID:86086150; PMID:3001109
A;Accession: A92755
A;Molecule type: DNA
A;Residues: 1-59,'N',61-205 <NED>
R;Iris, F.J.M.; Bougueleret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jurka
Nature Genet. 3, 137-145, 1993
A;Title: Dense Alu clustering and a potential new member of the NFkappaB family within a
A;Reference number: S36152; MUID:93272029; PMID:8499947
A;Accession: S36154
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-12,'R',14-205 <IRI>
A;Cross-references: EMBL:Z15026; NID:g37211; PIDN:CAA78746.1; PID:g37213
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
R;Abraham, L.J.; Du, D.C.; Zahedi, K.; Dawkins, R.L.; Whitehead, A.S.
Immunogenetics 33, 50-53, 1991
A;Title: Haplotypic polymorphisms of the TNFB gene.
A;Reference number: I54482; MUID:91139175; PMID:1671667
A;Accession: I54482
A;Status: translation not shown; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-124,'P',126-205 <RES>
A;Cross-references: GB:M55913; NID:g339742; PIDN:AAB59455.1; PID:g339743
A;Experimental source: ancestral haplotype 57.1
A;Note: 59-Asn was also found (ancestral haplotype 8.1)
R;Gray, P.W.; Aggarwal, B.B.; Benton, C.V.; Bringman, T.S.; Henzel, W.J.; Jarrett, J.A.;
Nature 312, 721-724, 1984
A;Title: Cloning and expression of cDNA for human lymphotoxin, a lymphokine with tumour
A;Reference number: A93350; MUID:85086243; PMID:6334807
A;Accession: A93350
A;Molecule type: mRNA
A;Residues: 1-205 <GRA>
A;Cross-references: GB:X01393; NID:g34444; PIDN:CAA25649.1; PID:g34445
A;Experimental source: lymphoblastoid cell line RPMI-1788
R;Goeddel, D.V.; Aggarwal, B.B.; Gray, P.W.; Leung, D.W.; Nedwin, G.E.; Palladino, M.A.;
Cold Spring Harb. Symp. Quant. Biol. 51, 597-609, 1986
A;Title: Tumor necrosis factors: gene structure and biological activities.
A;Reference number: A32877; MUID:87217059; PMID:3472740
A;Accession: B32877
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 35-205 <GOE>
R;Kobayashi, Y.; Miyamoto, D.; Asada, M.; Obinata, M.; Osawa, T.
J. Biochem. 100, 727-733, 1986
A;Title: Cloning and expression of human lymphotoxin mRNA derived from a human T cell
A;Reference number: A91906; MUID:87057135; PMID:3536896
A;Accession: A91906
A;Molecule type: mRNA
A;Residues: 1-59,'N',61-205 <KOB>
A;Cross-references: GB:D00102; NID:g219913; PIDN:BAA00064.1; PID:g219914
A;Note: the authors translated the codon TAT for residue 156 as Thr and ACC for resid
R;Fukuda, S.; Ando, S.; Sanou, O.; Taniai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.;
Lymphokine Res. 7, 175-185, 1988
A;Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta
A;Reference number: A61478; MUID:88301617; PMID:2841543
A;Accession: A61478
A;Molecule type: protein
A;Residues: 56-79;86-95,'X',97,'X',99;119-151,'XX',154-162,'X',164,'X',166,'X',168,'X
R;Voigt, C.G.; Maurer-Fogy, I.; Adolf, G.R.
FEBS Lett. 314, 85-88, 1992
A;Title: Natural human tumor necrosis factor beta (lymphotoxin). Variable O-glycosyla
A;Reference number: S26951; MUID:93083656; PMID:1451807
A;Accession: S26951
A;Molecule type: protein
A;Residues: 35-59,'N',61-205 <VOI>
A;Note: 60-Thr was also found
R;Fukushima, K.; Watanabe, H.; Takeo, K.; Nomura, M.; Asahi, T.; Yamashita, K.
Arch. Biochem. Biophys. 304, 144-153, 1993
A;Title: N-linked sugar chain structure of recombinant human lymphotoxin produced by
A;Reference number: S34742; MUID:93311995; PMID:8323280
A;Contents: annotation
C;Comment: Secreted from mitogen-activated lymphocytes within 1-2 days after inductio
while having no detrimental effect on normal cells. It can also act synergistically
C;Comment: This protein and TNF-alpha (tumor necrosis factor) are the products of dif
ical activities but are produced by different cell types and have different induction
C;Genetics:
A;Gene: GDB:LTA; LT; TNFB
A;Cross-references: GDB:120442; OMIM:153440
A;Map position: 6p21.3-6p21.3
A;Introns: 33/3; 69/1
A;Note: the first intron occurs before the initiator codon
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lymphokine; macrophage
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-205/Product: lymphotoxin #status predicted <MAT>
F;41/Binding site: carbohydrate (Thr) (covalent) (partial) #status experimental
F;96/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match   6.9%; Score 100.5; DB 1; Length 205;
  Best Local Similarity   23.6%; Pred. No. 0.35;
  Matches   51; Conservative   20; Mismatches   84; Indels   61; Gaps   9;

```
Qy         91 LPAGAGAPKAGLEEAPAVTA--------GLKIFEPPAPGEGN-SSQNSRNKRAVQGPEET 141
              ||   | |  ||  : | ||              :| |   |: | |||   ||    :
Db         29 LPGAQGLPGVGLTPSAAQTARQHPKMHLAHSTLKPAAHLIGDPSKQNSLLWRA--NTDRA 86

Qy        142 VTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEEKENKILVKETGYFFIYGQVLY 201
               ||   |                                  | :||  :| :|:| ||::
Db         87 FLQDGFSL-----------------------------SNNSLLVPTSGIYFVYSQVVF 115

Qy        202 TDKTYA----MGHLIQRKKVHVFGDELSLVTLFRCIQNMPETLPN------NSCYSAGIA 251
              : | |:       |    :| :|  :          | |    |        :| |
Db        116 SGKAYSPKATSSPLYLAHEVQLFSSQYPFHVPLLSSQKM--VYPGLQEPWLHSMYHGAAF 173

Qy        252 KLEEGDELQL---AIPRENAQISLDGDVTFFGALKL 284
              :| :||:|      ||     : |     |||  |
Db        174 QLTQGDQLSTHTDGIP----HLVLSPSTVFFGAFAL 205
```

RESULT 10
QWHUN
tumor necrosis factor alpha precursor [validated] - human
N;Alternate names: cachectin; TNFA
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 08-Dec-2000

C;Accession: A93585; S36153; A93351; A44189; B61478; I53311; S62610; I54522; A01646; B23
R;Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, D
Nucleic Acids Res. 13, 6361-6373, 1985
A;Title: Human lymphotoxin and tumor necrosis factor genes: structure, homology and chro
A;Reference number: A93585; MUID:86016093; PMID:2995927
A;Accession: A93585
A;Molecule type: DNA
A;Residues: 1-233 <NED>
A;Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210
R;Iris, F.J.M.; Bougueleret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jurka
Nature Genet. 3, 137-145, 1993
A;Title: Dense Alu clustering and a potential new member of the NFkappaB family within a
A;Reference number: S36152; MUID:93272029; PMID:8499947
A;Accession: S36153
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-233 <IRI>
A;Cross-references: EMBL:Z15026; NID:g37211; PIDN:CAA78745.1; PID:g37212
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
R;Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M.A.
Nature 312, 724-729, 1984
A;Title: Human tumour necrosis factor: precursor structure, expression and homology to l
A;Reference number: A93351; MUID:85086244; PMID:6392892
A;Accession: A93351
A;Molecule type: mRNA
A;Residues: 1-233 <PEN>
A;Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210
A;Note: this protein was isolated from the monocyte-like cell line HL-60 from a promyelo
R;Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdell, J.N.;
Science 228, 149-154, 1985
A;Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.
A;Reference number: A44189; MUID:85142190; PMID:3856324
A;Accession: A44189
A;Molecule type: mRNA
A;Residues: 1-62,'S',64-233 <WAN>
A;Cross-references: GB:M10988; NID:g339737; PIDN:AAA61198.1; PID:g339738
R;Fukuda, S.; Ando, S.; Sanou, O.; Taniai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; An
Lymphokine Res. 7, 175-185, 1988
A;Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and
A;Reference number: A61478; MUID:88301617; PMID:2841543
A;Accession: B61478
A;Molecule type: protein
A;Residues: 83-102;109-119;121-128,'X',130-131;142-144,'X',146,'XXX',150-152;159-174;180
R;Marmenout, A.; Fransen, L.; Tavernier, J.; Van Der Heyden, J.; Tizard, R.; Kawashima,
Eur. J. Biochem. 152, 515-522, 1985
A;Title: Molecular cloning and expression of human tumor necrosis factor and comparison
A;Reference number: I53311; MUID:86030296; PMID:3932069
A;Accession: I53311
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-233 <MAR>
A;Cross-references: GB:M26331; NID:g339763; PIDN:AAA36758.1; PID:g339764
A;Experimental source: U-937 cells
R;Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.
Eur. J. Biochem. 235, 431-437, 1996
A;Title: O-Glycosylated species of natural human tumor-necrosis factor-alpha.
A;Reference number: S62610; MUID:96202967; PMID:8631363
A;Accession: S62610
A;Molecule type: protein
A;Residues: 77-99 <TAK>
R;D'Alfonso, S.; Richiardi, P.M.
Immunogenetics 39, 150-154, 1994
A;Title: A polymorphic variation in a putative regulation box of the TNFA promoter regio
A;Reference number: I54522; MUID:94102809; PMID:7903959
A;Accession: I54522
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-8 <DAL>
A;Cross-references: GB:S68530; NID:g544751
R;Stevenson, F.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.
J. Exp. Med. 176, 1053-1062, 1992
A;Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific lys
A;Reference number: A59163; MUID:93018820; PMID:1402651
A;Contents: annotation; identification of myristylated lysines
R;Aggarwal, B.B.; Kohr, W.J.; Hass, P.E.; Moffat, B.; Spencer, S.A.; Henzel, W.J.; Br
J. Biol. Chem. 260, 2345-2354, 1985
A;Title: Human tumor necrosis factor. Production, purification, and characterization.
A;Reference number: A92511; MUID:85130974; PMID:3871770
A;Contents: annotation; disulfide bond
C;Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induct
out detriment to normal cells. It can also act synergistically with interferon gamma
C;Comment: TNF-alpha and -beta (lymphotoxin) are the products of different genes clos
ut are produced by different cell types and have different induction kinetics.
C;Genetics:
A;Gene: GDB:TNF; TNFA
A;Cross-references: GDB:120441; OMIM:191160
A;Map position: 6p21.3-6p21.3
A;Introns: 62/3; 78/1; 94/1
C;Complex: homotrimer
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein; lymphokine; m
F;1-76/Domain: propeptide #status predicted <PRO>
F;77-233/Product: tumor necrosis factor #status experimental <MAT>
F;19,20/Binding site: myristate (Lys) (covalent) #status experimental
F;81/Binding site: carbohydrate (Ser) (covalent) (partial) #status experimental
F;145-177/Disulfide bonds: #status experimental

Query Match 6.8%; Score 98.5; DB 1; Length 233;
Best Local Similarity 24.2%; Pred. No. 0.6;
Matches 44; Conservative 34; Mismatches 69; Indels 35; Gaps 9;

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Qy      135 VQGPEETVTQDCLQLI--------ADSETPTIQKGSYTF--------VPWLLSFKRGSAL 178
            | ||:       | ||        : | ||: :  ::          : ||   :| :||
Db       55 VIGPQREEFPRDLSLISPLAQAVRSSSRTPSDKPVAHVVANPQAEGQLQWL--NRRANAL 112

Qy      179 -----EEKENKILVKETGYFFIYGQVLYTDK----TYA-MGHLIQRKKVHVFGDELSLVT 228
                | ::|:::|   | : || |||:  :    |:  : | | |  |  :  :::|::
Db      113 LANGVELRDNQLVVPSEGLYLIYSQVLFKGQGCPSTHVLLTHTISRIAVS-YQTKVNLLS 171

Qy      229 LFR--CIQNMPETLPNNSCYS----AGIAKLEEGDELQLAIPRENAQISLDGDVTFFGAL 282
              :  | :  ||       |      |: :||:|| |   | | :     :    :|| :
Db      172 AIKSPCQRETPEGAEAKPWYEPIYLGGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGII 231

Qy      283 KL 284
             |
Db      232 AL 233
```

RESULT 11
A25451
tumor necrosis factor alpha precursor - rabbit
N;Alternate names: cachectin; TNF alpha
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C;Accession: A25454; A25451; JS0727
R;Ito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayashi,
DNA 5, 149-156, 1986
A;Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for
A;Reference number: A25454; MUID:86219711; PMID:3519137
A;Accession: A25454
A;Molecule type: mRNA
A;Residues: 1-234 <ITO>
A;Cross-references: GB:M12845; NID:g165759; PIDN:AAA31486.1; PID:g165760
R;Ito, H.; Shirai, T.; Yamamoto, S.; Akira, M.; Kawahara, S.; Todd, C.W.; Wallace, R.
DNA 5, 157-165, 1986
A;Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor.
A;Reference number: A25451; MUID:86219712; PMID:3519138
A;Accession: A25451
A;Molecule type: DNA
A;Residues: 1-234 <IT2>
A;Note: this sequence differs from that shown in having a Gln inserted between residu
R;Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.
Gene 95, 215-221, 1990
A;Title: Structural analysis of the rabbit TNF locus, containing the genes encoding T
A;Reference number: JH0309; MUID:91065534; PMID:2249779
A;Accession: JS0727

```
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-62,'Q',63-234 <SHA>
A;Cross-references: GB:M60340; GB:M35326; NID:g165754; PIDN:AAA31484.1; PID:g165756
C;Genetics:
A;Introns: 62/3; 80/1; 96/1
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; memb
F;1-81/Domain: propeptide #status predicted <PRO>
F;82-234/Product: tumor necrosis factor #status predicted <MAT>
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;83/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;147-178/Disulfide bonds: #status predicted

  Query Match             6.8%;  Score 98;  DB 1;  Length 234;
  Best Local Similarity   21.2%;  Pred. No. 0.67;
  Matches   49;  Conservative   46;  Mismatches   72;  Indels   64;  Gaps   13;

Qy        112 LKIFEPPAPGEGNSSQNSRNKRA----------------------VQGPEETVTQDCL 147
              ::: | | | :    | |  ||                      | ||:|  : : |
Db         10 VELAEGPLPKKAGGPQGS--KRCLCLSLFSFLLVAGATTLFCLLHFRVIGPQEEESPNNL 67

Qy        148 QLIAD-SETPTIQKGSYTF-----------------VPWLLSFKRGSAL-----EEKENK 184
               |:   ::  |::  |                    : ||   :| :||     :  :|:
Db         68 HLVNPVAQMVTLRSASRALSDKPLAHVVANPQVEGQLQWL--SQRANALLANGMKLTDNQ 125

Qy        185 ILVKETGYFFIYGQVLYTD---KTYA-MGHLIQRKKVHVFGDELSLVTLFR--CIQNMPE 238
              ::|   | : || |||::    ::|  : | : |  |  : ::::|::  :  | :  ||
Db        126 LVVPADGLYLIYSQVLFSGQGCRSYVLLTHTVSRFAVS-YPNKVNLLSAIKSPCHRETPE 184

Qy        239 TLPNNSCYS----AGIAKLEEGDELQLAIPR-ENAQISLDGDVTFFGALKL 284
                : |      |: :|||:|| |   : : |   ::  | | :|| : |
Db        185 EAEPMAWYEPIYLGGVFQLEKGDRLSTEVNQPEYLDLAESGQV-YFGIIAL 234


RESULT 12
A82993
hypothetical protein PA5225 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: A82993
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: A82993
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-184 <STO>
A;Cross-references: GB:AE004935; GB:AE004091; NID:g9951526; PIDN:AAG08610.1; GSPDB:GN001
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA5225

  Query Match             6.7%;  Score 97.5;  DB 2;  Length 184;
  Best Local Similarity   31.2%;  Pred. No. 0.55;
  Matches   35;  Conservative   11;  Mismatches   45;  Indels   21;  Gaps    4;

Qy         81 AELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAPGEGNSSQNSRNKRAVQGPEE 140
              ||| ||   :: ||||  :|  : | |   |        ||||       | | |: |
Db         25 AELHGHLLGRVCAGAGFDEAAWQHAAAELLG------GAPGE-------RLKAALSGLLG 71

Qy        141 TVTQD-------CLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEEKENKI 185
               | ||       : |: | |||  |: :     |   |  |  |  :|  :
Db         72 MVRQDFSAGEVAVVMLLPDDETPLAQR-TEALGQWCQGFLAGFGLTAREGSL 122


RESULT 13
I38707
Fas ligand - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Accession: I38707; JC2340; S57565; I38554
R;Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.
Int. Immunol. 6, 1567-1574, 1994
A;Title: Human Fas ligand: gene structure, chromosomal location and species specifici
A;Reference number: I38707; MUID:95127560; PMID:7826947
A;Accession: I38707
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-281 <RES>
A;Cross-references: EMBL:U11821; NID:g595430; PIDN:AAC50124.1; PID:g595431
R;Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamoto,
Biochem. Biophys. Res. Commun. 204, 468-474, 1994
A;Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.
A;Reference number: JC2340; MUID:95071350; PMID:7980502
A;Accession: JC2340
A;Molecule type: DNA
A;Residues: 1-281 <MIT>
A;Cross-references: GB:D38122; DDBJ:D29820; NID:g601892; PIDN:BAA07320.1; PID:g136990
R;Schatzlein, C.E.
submitted to the EMBL Data Library, June 1995
A;Reference number: S57565
A;Accession: S57565
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-281 <SCH>
A;Cross-references: EMBL:X89102; NID:g887455; PID:g887456
R;Alderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.;
J. Exp. Med. 181, 71-77, 1995
A;Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.
A;Reference number: I38554; MUID:95105731; PMID:7528780
A;Accession: I38554
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-281 <RE2>
A;Cross-references: EMBL:U08137; NID:g624627; PIDN:AAC50071.1; PID:g624628
C;Genetics:
A;Gene: FasL
A;Introns: 151/1; 116/3
C;Keywords: glycoprotein; transmembrane protein
F;80-102/Domain: transmembrane #status predicted <TMM>
F;76,184,250,260/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             6.7%;  Score 97.5;  DB 2;  Length 281;
  Best Local Similarity   20.7%;  Pred. No. 0.92;
  Matches   56;  Conservative   39;  Mismatches  107;  Indels   69;  Gaps   10;

Qy         31 LPRKESPSVR---SSKDGKLLAATLLLALLSCCLTVVSFYQVAALQGDLASLR-AELQGH 86
              ||    | ::   :   |  |     : |::     :  :|:  || :|| || :  | |
Db         63 LPPLPLPPLKKRGNHSTGLCLLVMFFMVLVALVGLGLGMFQLFHLQKELAELRESTSQMH 122

Qy         87 HAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAPGEGNSSQNSRNKRAVQGPEETVTQDC 146
               |  |    | |                  ||                   ||:   :
Db        123 TASSLEKQIGHP----------------SPP-----------------PEKKELRKV 146

Qy        147 LQLIADSET---PTIQKGSYTFVPWLLSFKRGSALEEKENKILVKETGYFFIYGQVLY-- 201
                |   | :   |   : :|  |  ||     | :: |:  ::: ||| :|:| :| :
Db        147 AHLTGKSNSRSMPLEWEDTYGIV--LL-----SGVKYKKGGLVINETGLYFVYSKVYFRG 199

Qy        202 --------TDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETLPNNSCYSAGIAKL 253
                     : | |       : | : |  :|  |  :         :   | |   :  |
Db        200 QSCNNLPLSHKVYMRNSKYPQDLVMMEGKMMSYCTTGQ--------MWARSSYLGAVFNL 251

Qy        254 EEGDELQLAIPRENAQISLDGDVTFFGALKL 284
                | | : :  | : :: :   ||||  ||
Db        252 TSADHLYVNV-SELSLVNFEESQTFFGLYKL 281


RESULT 14
A75537
hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
```

```
C;Accession: A75537
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: A75537
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-347 <WHI>
A;Cross-references: GB:AE001890; GB:AE000513; NID:g6457959; PIDN:AAF09880.1; PID:g645797
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR0288
A;Map position: 1

  Query Match             6.5%;  Score 94.5;  DB 2;  Length 347;
  Best Local Similarity   27.4%;  Pred. No. 2.2;
  Matches   37;  Conservative   23;  Mismatches   52;  Indels   23;  Gaps    5;

Qy          9 QSRLTSCLKKRE---EMKLKECVSILPRKESP-----SVRSSKDGKLLAATLLLALLSCC 60
              . |::  : |: ||    :  |: : :|| : :|     :  ||: || :::  |  | :
Db         99 QNQFRAALRAREGERTLNAKQFLKVLPAEGTPGRYLWNTISSEGGKAVSSRSLRTLGTAD 158

Qy         61 LTVVSFYQVAALQGD-------LASLRAELQGHHAEKL----PAG----AGAPKAGLEEA 105
                 ::|   |   |        || ::|||   ||| |    ||      | | ||  :
Db        159 GGTLTFQPEAVAAGTDPSVAALLAPVQAELARTHAELLAGLDPASFGLLRGGPAAGSPKP 218

Qy        106 PAVTAGLKIFEPPAP 120
                  ||  :||:|
Db        219 GQGFVRLKTLQPPSP 233


RESULT 15
RGBYD2
translation regulator GCD2 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein G4615; protein YGR083c
C;Species: Saccharomyces cerevisiae
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jun-2000
C;Accession: S05809; S64378
R;Paddon, C.J.; Hannig, E.M.; Hinnebusch, A.G.
Genetics 122, 551-559, 1989
A;Title: Amino acid sequence similarity between GCN3 and GCD2, positive and negative tra
A;Reference number: S05809; MUID:89339141; PMID:2668117
A;Accession: S05809
A;Molecule type: DNA
A;Residues: 1-651 <PAD>
A;Cross-references: EMBL:X15658; NID:g3733; PIDN:CAA33693.1; PID:g3734
R;Wedler, H.; Scharfe, M.; Wedler, E.; Wambutt, R.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64356
A;Accession: S64378
A;Molecule type: DNA
A;Residues: 1-651 <WED>
A;Cross-references: EMBL:Z72868; NID:g1323118; PIDN:CAA97085.1; PID:g1323119; GSPDB:GN00
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:GCD2; GCD12; MIPS:YGR083c
A;Cross-references: SGD:S0003315; MIPS:YGR083c
A;Map position: 7R
C;Superfamily: translation regulator GCD2
C;Keywords: P-loop; phosphoprotein
F;573-580/Region: nucleotide-binding motif A (P-loop) #status atypical
F;106/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predic
F;121/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predic

  Query Match             6.4%;  Score 93.5;  DB 1;  Length 651;
  Best Local Similarity   19.1%;  Pred. No. 5.7;
  Matches   67;  Conservative   55;  Mismatches  140;  Indels   89;  Gaps   15;

Qy          2 DDSTEREQSRLTSCLKKREEMKLKECVSI--LPRKE---------SPSVRSSKDGKLLAA 50
              :   :||| :  :  ||: |  :|:      |   |         : :| | |  :: ||

Db         81 EQQQKREQKQKNANKKKQNERNVKKSTLFGHLETTEERRATILALTSAVSSPKTSRITAA 140

Qy         51 TLLLALLSCCLTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTA 110
              |:: :::           :|| |      : |       :| |  |          ||| |
Db        141 GLMVPVVA-----------SALSGSNVLTASSL-------MPVGPNASSTVSASAPASTT 182

Qy        111 GLKIFEPPAPGEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWL- 169
                  |   | || ::    |:|  :|  : :   :     : ::: | :  :| :
Db        183 TTLPASSAALSAGTSSASTNTPTAIQ--QEIASSNASDVAKTLASISLEAGEFNVIPGIS 240

Qy        170 --------LSFKRGSALEE-KE---NK--------ILVKETGYFFIYG------------ 197
                     ||   | :   ||   ||        :|     :: | |
Db        241 SVIPTVLEQSFDNSSLISSVKELLLNKDLIHPSILLLTSHLAHYKIVGSIPRCIAMLEVF 300

Qy        198 QVLYTDKTYAMGHLIQRKKVHVFGDELSL--------VTLFRCIQNMPETL-------PN 242
              |::  |    |  : |         :: |        ||:   |: : : :       |:
Db        301 QIVIKDYQTPKGTTLSRNLTSYLSHQIDLLKKARPLSVTMGNAIRWLKQEISLIDPSTPD 360

Qy        243 NS-----CYSAG---IAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
              :     |   |      |:|  |  || |   : ||      :  :|: |:|
Db        361 KAAKKDLCEKIGQFAKEKIELAD--QLIIDNASTQIEESTTIVTYGSSKVL 409


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Job time : 42 secs
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